

## BLAST Basic Local Alignment Search Tool

- Your search is limited to records matching **entrez** query: Homo sapiens [ORGN].

Edit and Resubmit Save Search Strategies Formatting options Download

## Protein Sequence (430 letters)

Results for: [cd|24806 None(430aa) ▼]

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

## Query ID

cd|24806

## Description

None

## Molecule type

amino acid

## Query Length

430

## Database Name

nr

## Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

## Program

BLASTP 2.2.19+ Citation

## Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Woitton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

## Search Parameters

|                         |          |
|-------------------------|----------|
| Program                 | blastp   |
| Word size               | 3        |
| Expect value            | 10       |
| Hits/size               | 100      |
| Gapcosts                | 11,1     |
| Matrix                  | BL0SUM62 |
| Threshold               | 11       |
| Composition-based stats | 2        |
| Filter string           | F        |
| Genetic Code            | 1        |
| Window Size             | 40       |

## Database

|                     |                      |
|---------------------|----------------------|
| Posted date         | Feb 12, 2009 6:03 PM |
| Number of letters   | 2,713,143,868        |
| Number of sequences | 7,873,120            |
| Entrez query        | Homo sapiens [ORGN]  |

## Karlin-Altschul statistics

| Params | Un-gapped | Gapped |
|--------|-----------|--------|
| Lambda | 0.326046  | 0.267  |
| K      | 0.138029  | 0.041  |
| H      | 0.443787  | 0.14   |

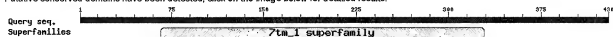
## Results Statistics

|                              |             |
|------------------------------|-------------|
| Length adjustment            | 115         |
| Effective length of query    | 315         |
| Effective length of database | 54918291    |
| Effective search space       | 17295261665 |
| Effective search space used  | 17295261665 |

## Graphic Summary

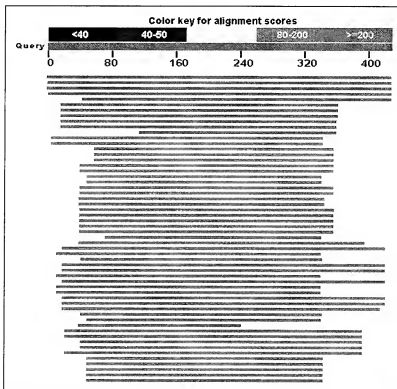
## Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



## Distribution of 104 Blast Hits on the Query Sequence

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

| Sequences producing significant alignments:                       | Score<br>(Bits) | E<br>Value |
|---|-----------------|------------|
| ref NP_071429.1  neuropeptide FF receptor 1 [Homo sapiens] >...   | 881             | 0.0        |
| ref BAC05950.1  seven transmembrane helix receptor [Homo sapiens] | 880             | 0.0        |
| gb AK941199.1 AF330055_1 neuropeptide NPYV receptor [Homo sap...] | 880             | 0.0        |
| emb CA112599.1  neuropeptide FF receptor 1 [Homo sapiens]         | 877             | 0.0        |
| gb EAW54387.1  neuropeptide FF receptor 1 [Homo sapiens]          | 789             | 0.0        |
| ref NP_444264.1  neuropeptide FF receptor 2 isoform 2 [Homo s...] | 423             | 7e-118     |
| ref NP_001138228.1  neuropeptide FF receptor 2 isoform 3 [Hom...] | 422             | 1e-117     |
| gb AAK58513.1 AP236083_1 G-protein-coupled receptor 74 [Homo ...] | 422             | 2e-117     |
| gb AAD22047.1  G-protein-coupled receptor [Homo sapiens]          | 420             | 4e-117     |
| ref NP_004876.2  neuropeptide FF receptor 2 isoform 1 [Homo s...] | 420             | 4e-117     |
| gb EAK05647.1  neuropeptide FF receptor 2, isoform CRA_a [Hom...] | 286             | 1e-76      |
| ref NP_001517.2  orexin receptor 2 [Homo sapiens] >sp O43614....  | 190             | 7e-48      |
| gb AAC39602.1  orexin receptor-2; OX2R; G protein-coupled rec...  | 190             | 7e-48      |
| gb AAC39601.1  orexin receptor-1; OX1R; G protein-coupled rec...  | 181             | 4e-45      |
| ref NP_001516.2  orexin receptor 1 [Homo sapiens] >sp O43613....  | 179             | 2e-44      |
| dbj BAF83210.1  unnamed protein product [Homo sapiens]            | 179             | 2e-44      |
| ref NP_009091.1  neuropeptide Y receptor Y2 [Homo sapiens] >...   | 167             | 9e-41      |
| gb AAA93170.1  type 2 neuropeptide Y receptor                     | 165             | 3e-40      |
| ref NP_937822.2  G protein-coupled receptor 103 [Homo sapiens]... | 165             | 3e-40      |
| dbj BAC98938.1  ORP2 receptor [Homo sapiens]                      | 164             | 4e-40      |
| gb AAD00248.1  neuropeptide Y receptor type 2 [Homo sapiens]      | 164             | 5e-40      |
| gb AA807760.1  neuropeptide y/peptide YY receptor type 2          | 164             | 6e-40      |
| gb AAAS9920.1  neuropeptide y receptor                            | 160             | 8e-39      |
| ref NP_000900.1  neuropeptide Y receptor Y1 [Homo sapiens] >...   | 160             | 1e-38      |
| gb AA473705.1 AP236081_1 orphan G-protein coupled receptor GP...  | 156             | 1e-37      |
| sp Q9NYM4.2 GPR83_HUMAN RecName: Full=Probable G-protein cou...   | 156             | 1e-37      |
| ref NP_057624.2  G protein-coupled receptor 83 [Homo sapiens]...  | 156             | 1e-37      |
| dbj BAH96064.1  KIAA1540 protein [Homo sapiens]                   | 156             | 1e-37      |
| gb AAH67474.1  G protein-coupled receptor 83 [Homo sapiens]       | 152             | 2e-36      |
| gb AAI28134.1  GPR103 protein [Homo sapiens]                      | 149             | 2e-35      |
| ref NP_003848.1  galanin receptor 2 [Homo sapiens] >sp O43603.... | 148             | 3e-35      |
| gb AA805897.1  neurokinin-2 receptor                              | 148             | 4e-35      |
| gb AAH99637.1  Pancreatic polypeptide receptor 1 [Homo sapiens]   | 148             | 4e-35      |
| ref NP_000721.1  cholecystokinin A receptor [Homo sapiens] >...   | 147             | 8e-35      |
| sp P21452.2 NK2R_HUMAN RecName: Full=Substance-K receptor; Sh...  | 146             | 1e-34      |
| gb AAC31760.1  neurokinin A receptor [Homo sapiens] >gb AAA60.... | 145             | 3e-34      |
| ref NP_005963.3  pancreatic polypeptide receptor 1 [Homo sapiens] | 145             | 3e-34      |
| ref NP_001048.2  tachykinin receptor 2 [Homo sapiens] >dbj BA.... | 145             | 3e-34      |
| gb AA807759.1  pancreatic polypeptide receptor >gb AAV68196.1.... | 145             | 3e-34      |
| emb CAG46748.1  PPYR1 [Homo sapiens]                              | 143             | 9e-34      |
| gb EAW54325.1  tachykinin receptor 2, isoform CRA_b [Homo sap...] | 142             | 3e-33      |
| gb AAH6842.1  Tachykinin receptor 2 [Homo sapiens]                | 140             | 9e-33      |
| gb AAH20304.1  substance K receptor, SR receptor [human, Pep...]  | 139             | 2e-32      |
| prf 121182212  cholecystokinin A receptor                         | 137             | 6e-32      |
| gb AAI26488.1 AP41117.1 G protein-coupled receptor [Homo sap...]  | 135             | 3e-31      |
| dbj AAD92474.1  neuropeptide Y receptor Y1 variant [Homo sapi...] | 127             | 9e-29      |
| gb AAI22552.1  Tachykinin receptor 3 [Homo sapiens]               | 125             | 2e-28      |
| gb AAH21706.1  neurokinin-3 receptor; NK-3 receptor [Homo sap...] | 125             | 2e-28      |
| emb CAA46291.1  neuremodin K receptor [Homo sapiens]              | 125             | 3e-28      |
| ref NP_001050.1  tachykinin receptor 3 [Homo sapiens] >sp P29.... | 125             | 3e-28      |
| gb AAH95527.1  TACR3 protein [Homo sapiens]                       | 124             | 7e-28      |
| sp Q13585.1 MTLR1_HUMAN RecName: Full=Melatonin-related recep...  | 123             | 1e-27      |
| ref NP_004215.2  G protein-coupled receptor 50 [Homo sapiens]     | 123             | 1e-27      |
| gb AAI03697.1  GPR50 protein [Homo sapiens] >gb AAI05684.1  G...  | 122             | 2e-27      |
| gb AAI05685.1  G protein-coupled receptor 50 [Homo sapiens] >...  | 122             | 2e-27      |
| gb EAW9402.1  G protein-coupled receptor 50 [Homo sapiens]        | 122             | 2e-27      |
| ref NP_001718.1  bombesin-like receptor 3 [Homo sapiens] >sp ...  | 122             | 2e-27      |
| emb CAG46720.1  DRD1 [Homo sapiens]                               | 122             | 2e-27      |
| ref NP_001471.2  galanin receptor 1 [Homo sapiens]                | 122             | 2e-27      |
| sp P47211.1 GALR1_HUMAN RecName: Full=Galanin receptor type 1...  | 122             | 2e-27      |
| emb CAA41734.1  D-1 dopamine receptor [Homo sapiens]              | 122             | 2e-27      |
| gb AAK93235.1 AP343725_1 G-protein-coupled receptor GPR54 [Ho...  | 122             | 2e-27      |

|                 |  |     |       |            |
|-----------------|--|-----|-------|------------|
| gb EAW61376.1   | dopamine receptor D1, isoform CRA_a [Homo sapiens]           | 122 | 2e-27 | <b>G</b>   |
| ref NP_000785.1 | dopamine receptor D1 [Homo sapiens]                          | 122 | 2e-27 | <b>U G</b> |
| gb AAB60356.1   | galanin receptor >gb AAC95397.1  galanin receptor            | 122 | 3e-27 | <b>G</b>   |
| ref NP_115940.2 | G protein-coupled receptor 54 [Homo sapiens]                 | 122 | 3e-27 | <b>U G</b> |
| prf 11614340A   | dopamine receptor D1   | 120 | 6e-27 |            |
| gb BAG36078.1   | unnamed protein product [Homo sapiens]                       | 117 | 5e-26 | <b>G</b>   |
| ref NP_001041.1 | somatostatin receptor 2 [Homo sapiens]                       | 117 | 8e-26 | <b>U G</b> |
| gb AAA20828.1   | somatostatin receptor  | 117 | 8e-26 | <b>G</b>   |
| ref NP_001044.1 | somatostatin receptor 5 [Homo sapiens]                       | 117 | 9e-26 | <b>U G</b> |
| ref NP_004239.1 | G protein-coupled receptor 10 [Homo sapiens]                 | 117 | 9e-26 | <b>U G</b> |
| gb AAF42810.1   | AF184174_2 somatostatin receptor 2B [Homo sapiens]           | 116 | 1e-25 | <b>G</b>   |
| ref NP_658986.1 | prokineticin receptor 2 [Homo sapiens]                       | 116 | 1e-25 | <b>U G</b> |
| gb EAX10422.1   | prokineticin receptor 2 [Homo sapiens]                       | 116 | 2e-25 | <b>G</b>   |
| dbj BAG36594.1  | unnamed protein product [Homo sapiens]                       | 116 | 2e-25 | <b>G</b>   |
| gb AAH95542.1   | Neuromedin B receptor [Homo sapiens]                         | 115 | 2e-25 | <b>G</b>   |
| gb ABQ52418.1   | prokineticin receptor 2 [Homo sapiens]                       | 115 | 2e-25 | <b>G</b>   |
| ref NP_002502.2 | neuromedin B receptor [Homo sapiens]                         | 115 | 3e-25 | <b>U G</b> |
| gb AAAS9939.1   | neuromedin B receptor >gb AAB27330.1  neuromedin B           | 115 | 3e-25 | <b>G</b>   |
| gb AA336623.1   | somatostatin receptor >dbj BAA04106.1  fourth                | 115 | 4e-25 | <b>G</b>   |
| gb AAK61266.1   | AB006466_1 somatostatin receptor type 5 [Homo sapiens]       | 115 | 4e-25 | <b>G</b>   |
| ref NP_005959.1 | melatonin receptor 1B [Homo sapiens]                         | 114 | 6e-25 | <b>U G</b> |
| ref AAH09522.1  | AAH09522 Unknown (protein for IMAGE:3354783) [Homo sapiens]  | 114 | 9e-25 | <b>G</b>   |
| ref NP_001043.2 | somatostatin receptor 4 [Homo sapiens]                       | 113 | 1e-24 | <b>U G</b> |
| gb AAN87342.1   | DRG kappa 1 splice variant KOR 1A [Homo sapiens]             | 113 | 1e-24 | <b>G</b>   |
| gb EAX10169.1   | somatostatin receptor 4, isoform CRA_b [Homo sapiens]        | 113 | 1e-24 | <b>G</b>   |
| emb CAB73066.1  | prolactin releasing hormone receptor [Homo sapiens]          | 113 | 1e-24 | <b>G</b>   |
| dbj BAF82684.1  | unnamed protein product [Homo sapiens]                       | 113 | 1e-24 | <b>G</b>   |
| gb AAA60565.1   | somatostatin receptor  | 112 | 2e-24 | <b>G</b>   |
| dbj BAG60542.1  | unnamed protein product [Homo sapiens]                       | 110 | 6e-24 | <b>G</b>   |
| gb AAM21070.1   | AF498922_1 opioid receptor kappa [Homo sapiens]              | 110 | 6e-24 | <b>G</b>   |
| ref NP_000903.2 | opioid receptor, kappa 1 [Homo sapiens]                      | 110 | 7e-24 | <b>U G</b> |
| gb AAN32829.1   | AF441129_1 cholecystokinin-C receptor [Homo sapiens]         | 110 | 8e-24 | <b>G</b>   |
| gb EAW68734.1   | cholecystokinin B receptor, isoform CRA_a [Homo sapiens]     | 110 | 1e-23 | <b>G</b>   |
| gb EAX05261.1   | G protein-coupled receptor 103, isoform CRA_a [Homo sapiens] | 110 | 1e-23 | <b>G</b>   |
| ref NP_795344.1 | cholecystokinin B receptor [Homo sapiens]                    | 110 | 1e-23 | <b>U G</b> |
| gb AAB30766.2   | cholecystokinin B receptor [Homo sapiens]                    | 109 | 1e-23 | <b>G</b>   |
| ref NP_001040.1 | somatostatin receptor 1 [Homo sapiens]                       | 109 | 1e-23 | <b>U G</b> |
| gb EAW68735.1   | cholecystokinin B receptor, isoform CRA_b [Homo sapiens]     | 109 | 2e-23 | <b>G</b>   |

Alignments Select All Get selected sequences Distance tree of results

```

>ref|NP_071429.1| U G neuropeptide FF receptor 1 [Homo sapiens]
sp|G5QZG6.1|NPFF1_HUMAN G RecName: Full=Neuropeptide FF receptor 1; AltName: Full=G-protein
coupled receptor 147; AltName: Full=RFamide-related peptide
receptor OT77022
gb|AAG41397.1|AF268098_1 G neuropeptide FF receptor 1 [Homo sapiens]
dbj|BAB17677.1| G RFamide-related peptide receptor [Homo sapiens]
gb|AAI31581.1| G Neuropeptide FF receptor 1 [Homo sapiens]
gb|ABY87927.1| G neuropeptide FF receptor 1 [Homo sapiens]
Length=430
GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]
(10 or fewer PubMed links)
Score = 881 bits (2276), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 430/430 (100%), Positives = 430/430 (100%), Gaps = 0/430 (0%)

Query 1 MEGEPQSPNNSPLQSGNTQTEATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 60
Sbjct 1 MEGEPQSPNNSPLQSGNTQTEATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 60
Query 61 NTLVCFIVLKNRHHMTVTNNFILNLAVSDLLVGI FCMPTTLVDNLITGWPFEDNATCRMSG 120
Sbjct 61 NTLVCFIVLKNRHHMTVTNNFILNLAVSDLLVGI FCMPTTLVDNLITGWPFEDNATCRMSG 120
Query 121 LVQMSVSASVFTLVATIAVERFRCI VHPFREKLTLRKALVTIAVIMALLIMCPSAVTL 180
Sbjct 121 LVQMSVSASVFTLVATIAVERFRCI VHPFREKLTLRKALVTIAVIMALLIMCPSAVTL 180
Query 181 TVTRESHHMPVDANNRSYFLYSCEAWPEKGRNVYTVLFSHYLAPLALIVMVYARIA 240
Sbjct 181 TVTRESHHMPVDANNRSYFLYSCEAWPEKGRNVYTVLFSHYLAPLALIVMVYARIA 240
Query 241 RKLCAQPGAPGGEAADPRASRRRVRVHMLVVALFPTLSWPLWALLLLIDYQGLSA 300
Sbjct 241 RKLCAQPGAPGGEAADPRASRRRVRVHMLVVALFPTLSWPLWALLLLIDYQGLSA 300

```

Query 301 PQLHLVTYVAPFFAHMLAFNSSANPIIYGYNENFRGQQAARLCRPPSGSHKEAY 360  
 Sbjct 301 PQLHLVTYVAPFFAHMLAFNSSANPIIYGYNENFRGQQAARLCRPPSGSHKEAY 360  
 Query 361 SERPQGLLHRRVFPVVRPSDGLPSSGSPSSGAPRGRPLRNGRVAHGLPREGPCSH 420  
 Sbjct 361 SERPQGLLHRRVFPVVRPSDGLPSSGSPSSGAPRGRPLRNGRVAHGLPREGPCSH 420  
 Query 421 LPLTIPAWDI 430  
 Sbjct 421 LPLTIPAWDI 430

>dbj|BAC05950.1| G seven transmembrane helix receptor [Homo sapiens]  
 Length=441  
 GENE ID: 64105 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
 (10 or fewer PubMed links)  
 Score = 880 bits (2274), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 429/429 (100%), Positives = 429/429 (100%), Gaps = 0/429 (0%)  
 Query 2 EGEPSPQPNSSWFLSQNGTNTATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 61  
 Sbjct 13 EGEPSPQPNSSWFLSQNGTNTATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 72  
 Query 62 TLVCFVLKRNHRHGTVTNMFILNLAVSDLLVGICMPTTLVDNLITGNFMDNATCKMSGL 121  
 Sbjct 73 TLVCFVLKRNHRHGTVTNMFILNLAVSDLLVGICMPTTLVDNLITGNFMDNATCKMSGL 132  
 Query 122 VQMGVSASVFTLVAIAVERFCRIVHPFREKILTKALVTIAIWAALILMCPASVTLT 181  
 Sbjct 133 VQMGVSASVFTLVAIAVERFCRIVHPFREKILTKALVTIAIWAALILMCPASVTLT 192  
 Query 182 VTREHHPMVDARNRSYPLVSCWEAMPEKMRVTVTVLPSHILAPLALIVVMYARIAR 241  
 Sbjct 193 VTREHHPMVDARNRSYPLVSCWEAMPEKMRVTVTVLPSHILAPLALIVVMYARIAR 252  
 Query 242 KLCAQPGAPGGEAADPRASRRRARRVHMLVMVALFPTLSWLPKALLLLIDYQQLSAP 301  
 Sbjct 253 KLCAQPGAPGGEAADPRASRRRARRVHMLVMVALFPTLSWLPKALLLLIDYQQLSAP 312  
 Query 302 QLHLVTYVAPFFAHMLAFNSSANPIIYGYNENFRGQQAARLCRPPSGSHKEAYS 361  
 Sbjct 313 QLHLVTYVAPFFAHMLAFNSSANPIIYGYNENFRGQQAARLCRPPSGSHKEAYS 372  
 Query 362 ERPGQLLHRRVFPVVRPSDGLPSSGSPSSGAPRGRPLRNGRVAHGLPREGPCSHL 421  
 Sbjct 373 ERPGQLLHRRVFPVVRPSDGLPSSGSPSSGAPRGRPLRNGRVAHGLPREGPCSHL 432  
 Query 422 LPLTIPAWDI 430  
 Sbjct 421 LPLTIPAWDI 441

>gb|AAK94199.1|AF330055.1 G neuropeptide NPVF receptor [Homo sapiens]  
 Length=430  
 GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
 (10 or fewer PubMed links)  
 Score = 880 bits (2273), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 429/430 (99%), Positives = 429/430 (99%), Gaps = 0/430 (0%)  
 Query 1 MESEPQPNSSWFLSQNGTNTATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 60  
 Sbjct 1 MESEPQPNSSWFLSQNGTNTATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 60  
 Query 61 NTLVCFVLKRNHRHGTVTNMFILNLAVSDLLVGICMPTTLVDNLITGNFMDNATCKMSG 120  
 Sbjct 61 NTLVCFVLKRNHRHGTVTNMFILNLAVSDLLVGICMPTTLVDNLITGNFMDNATCKMSG 120  
 Query 121 LVQMGVSASVFTLVAIAVERFCRIVHPFREKILTKALVTIAIWAALILMCPASVTL 180  
 Sbjct 121 LVQMGVSASVFTLVAIAVERFCRIVHPFREKILTKALVTIAIWAALILMCPASVTL 180  
 Query 181 TVTREHHPMVDARNRSYPLVSCWEAMPEKMRVTVTVLPSHILAPLALIVVMYARIAR 240  
 Sbjct 181 TVTREHHPMVDARNRSYPLVSCWEAMPEKMRVTVTVLPSHILAPLALIVVMYARIAR 240  
 Query 241 KLCAQPGAPGGEAADPRASRRRARRVHMLVMVALFPTLSWLPKALLLLIDYQQLSAP 300  
 Sbjct 241 KLCAQPGAPGGEAADPRASRRRARRVHMLVMVALFPTLSWLPKALLLLIDYQQLSAP 300  
 Query 301 PQLHLVTYVAPFFAHMLAFNSSANPIIYGYNENFRGQQAARLCRPPSGSHKEAY 360  
 Sbjct 301 PQLHLVTYVAPFFAHMLAFNSSANPIIYGYNENFRGQQAARLCRPPSGSHKEAY 360  
 Query 361 SERPQGLLHRRVFPVVRPSDGLPSSGSPSSGAPRGRPLRNGRVAHGLPREGPCSH 420  
 Sbjct 361 SERPQGLLHRRVFPVVRPSDGLPSSGSPSSGAPRGRPLRNGRVAHGLPREGPCSH 420  
 Query 421 LPLTIPAWDI 430  
 Sbjct 421 LPLTIPAWDI 430

>emb|CAI12599.1| G neuropeptide FF receptor 1 [Homo sapiens]  
 Length=428  
 GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
 (10 or fewer PubMed links)  
 Score = 877 bits (2265), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 428/428 (100%), Positives = 428/428 (100%), Gaps = 0/428 (0%)  
 Query 3 EGEPSPQPNSSWFLSQNGTNTATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 62  
 Sbjct 3 EGEPSPQPNSSWFLSQNGTNTATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCMVG 62

Sbjct 1 GEPGQPNSMPLSQNGTHTTEATPATNLTPSSYQHTSPVAAMFIVAYALIFLLCHVGMT 60

Query 63 LVCFIVLKNRHMHTVTNMFILNLAVALSDLLVGIFCMPTTLVDNLTGWPFNDNATCMSGLV 122

Sbjct 61 LVCFIVLKNRHMHTVTNMFILNLAVALSDLLVGIFCMPTTLVDNLTGWPFNDNATCMSGLV 120

Query 123 QGMSVSASVFTLVAIAVERFCRIVHPFREKLTKALKATVIAIVAILLIMCPSAVTLTV 182

Sbjct 121 QGMSVSASVFTLVAIAVERFCRIVHPFREKLTKALKATVIAIVAILLIMCPSAVTLTV 180

Query 183 TREEHFMVDANKRSYPLYSWCWAEPEKGRKRVVTVLFSHIYLAFLALIVMYARIARK 242

Sbjct 181 TREEHFMVDANKRSYPLYSWCWAEPEKGRKRVVTVLFSHIYLAFLALIVMYARIARK 240

Query 243 LCAQGPAPGGEAADPRASRRARVVMHVMVALFPTLSWLPLWALLLLIDYGQLSAQ 302

Sbjct 241 LCAQGPAPGGEAADPRASRRARVVMHVMVALFPTLSWLPLWALLLLIDYGQLSAQ 300

Query 303 LHLVTVYAPFPAHILAFFNSANPIIYGYNFENFRGQAAFRKLCRPRSGSHKEAYSE 362

Sbjct 301 LHLVTVYAPFPAHILAFFNSANPIIYGYNFENFRGQAAFRKLCRPRSGSHKEAYSE 360

Query 363 RGGLLHRVYVVPVRPSDGLPESGSPSSGAPRGRPLRNGRVANHGLPREGPGCSHLP 422

Sbjct 361 RGGLLHRVYVVPVRPSDGLPESGSPSSGAPRGRPLRNGRVANHGLPREGPGCSHLP 420

Query 423 LTIIPAWDI 430

Sbjct 421 LTIIPAWDI 428

-gb|EAW54387.1| **G** neuropeptide FF receptor 1 [Homo sapiens]  
Length=386

GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 789 bits (2037), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 386/386 (100%), Positives = 386/386 (100%), Gaps = 0/386 (0%)

Query 45 MFIVAYALIFLLCHVGMTLVCFIVLKNRHMHTVTNMFILNLAVALSDLLVGIFCMPTTLVDN 104

Sbjct 1 MFIVAYALIFLLCHVGMTLVCFIVLKNRHMHTVTNMFILNLAVALSDLLVGIFCMPTTLVDN 60

Query 105 LTGWPFNDNATCMSGLVQGMVSASVFTLVAIAVERFCRIVHPFREKLTKALKATVIAV 164

Sbjct 103 LTGWPFNDNATCMSGLVQGMVSASVFTLVAIAVERFCRIVHPFREKLTKALKATVIAV 120

Query 165 IWALLLIMCPSAVTLTVTREHHFMVDANKRSYPLYSWCWAEPEKGRKRVVTVLFSHI 224

Sbjct 121 IWALLLIMCPSAVTLTVTREHHFMVDANKRSYPLYSWCWAEPEKGRKRVVTVLFSHI 180

Query 225 YIAPLALIVMYARIARKLCAQGPAPGGEAADPRASRRARVVMHVMVALFPTLSWL 284

Sbjct 181 YIAPLALIVMYARIARKLCAQGPAPGGEAADPRASRRARVVMHVMVALFPTLSWL 240

Query 285 PLWALLLLIDYGQLSAQPLHLTVYAPFPAHILAFFNSANPIIYGYNFENFRGQAAFR 344

Sbjct 241 PLWALLLLIDYGQLSAQPLHLTVYAPFPAHILAFFNSANPIIYGYNFENFRGQAAFR 300

Query 345 RARLCRPRSGSHKEAYSERPGGLLRHVYVVPVRPSDGLPESGSPSSGAPRGRPLRNG 404

Sbjct 301 RARLCRPRSGSHKEAYSERPGGLLRHVYVVPVRPSDGLPESGSPSSGAPRGRPLRNG 360

Query 405 RVANHGLPREGPGCSHLPITIPAWDI 430

Sbjct 361 RVANHGLPREGPGCSHLPITIPAWDI 386

>ref|NP\_444264.1| **UG** neuropeptide FF receptor 2 isoform 2 [Homo sapiens]

gb|AAF87078.1|AF257210.1 **G** G-protein coupled receptor HLWAT7 [Homo sapiens]

gb|AAG41396.1|AF268899.1 **G** neuropeptide FF receptor 2 [Homo sapiens]

gb|AAK94197.1|AF330053.1 **G** neuropeptide NPFF receptor [Homo sapiens]

gb|EAX05648.1| **G** neuropeptide FF receptor 2, isoform CRA\_b [Homo sapiens]

gb|AAI13714.2| **G** Neuropeptide FF receptor 2 [Homo sapiens]

gb|AAI01637.1| **G** Neuropeptide FF receptor 2 [Homo sapiens]

dbj|BAF83626.1| **G** unnamed protein product (Homo sapiens)  
Length=420

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 423 bits (1087), Expect = 7e-118, Method: Compositional matrix adjust.  
Identities = 197/348 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)

Query 18 NGTMTTEATPATNLTPSSYQHTSPVAAMFIVAYALIFLLCHVGMTLVCFIVLKNRHMHTV 77

Sbjct 20 NUTKHLIYSDIITVNTLHQPOVAIIFISYVILFLLCHVGMTLVCFIVLKNRHMHTV 79

Query 78 TMLFNLNLAVALSDLLVGIFCMPTTLVDNLTGWPFNDNATCMSGLVQGMVSASVFTLVAI 137

Sbjct 80 TMLFNLNLAVALSDLLVGIFCMPTTLVDNLTGWPFNDNATCMSGLVQGMVSASVFTLVAI 139

Query 138 AVERFCRIVHPFREKLTKALKATVIAIVAILLIMCPSAVTLTVTREHHFMVDANKRS 196

Sbjct 140 AVERFCRIVHPFREKLTKALKATVIAIVAILLIMCPSAVTLTVTREHHFMVDANKRS 199

Query 197 SYPLYSWCWAEPEKGRKRVVTVLFSHIYIAPLALIVMYARIARKLCAQGPAPGGEA 256

Sbjct 200 TSPVYHRCEDPNQGRKRYITVLFANIYLAFLSLIVINRGISLRAVAFGRNGR 259

Query 257 ADPR-ASRRARVVMHVMVALFPTLSWLPLWALLLLIDYGQLSAQPLHLTVYAPFPAH 315

Sbjct 260 EQHNRVSRKQKIKNLLIALLVALLFSLWFLPLTAMLSYADLSPNQLQINIIYVPPAH 319

Query 316 WLAFNSSANPIIYGFNFNFRGQFAAFARLCPRPSGSHKEAYSER 363  
 Sbjct 320 WLAF NSS NPIIYG-FNFNFRGQ AF+ +LC + + EAY+ +  
 WLAFGSSVNPIIYGFNFNFRGQFAAFQQLQCKRAKP-MEAYALK 366

>ref|NP\_001138228.1| [C] neuropeptide FF receptor 2 isoform 3 [Homo sapiens]  
 gi|BA05650.1| [C] neuropeptide FF receptor 2, isoform CRA\_d [Homo sapiens]  
 Length=423

GENE ID: 10886 NPFRF2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 422 bits (1085), Expect = 1e-117, Method: Compositional matrix adjust.  
 Identities = 197/344 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)  
 Query 18 NGTNTTEATPATNLTFSSYQHTSPVAAMFIVAYAILFLCKMGNTLVCFVLKRNHMTV 77  
 N T N+T+ +Y H VAA-FI++Y LIF LCM-GNT+VCFIV++N+HMTV  
 Sbjct 23 NDTKHLHLYSDINITYVNYLHQVQAAIFIIISYFLFLCKMGNTVVCFIVMRKNHMTV 82  
 Query 78 TNMFLINLAUSDLLGIFCMPTTLVDMLITGWPFNDKATCMGSLVQGMVSASVFTLVAI 137  
 TN+FLINLA+SDLLGIFCMPT TL+DN+I GWPF N CK+SLGVQ+SV+ASVFTLVAI  
 Sbjct 83 TNLFLINLAISDLLGIFCMPTILLDNIAGWPFNTCKISGLVQGISVAASVFTLVAI 142  
 Query 138 AVFRFCIVHPFPEKLTIRKALVTIAVWALALLIMCPSAVLTITVREEHFM-VDARRN 196  
 AV+RF+C+V+PF+ KLT++ A V I +W LA+ IM PSV L V E+++ + +++N+  
 Sbjct 143 AVDRFCQVVPFPEKLTITKTAFTVIMIIWVLAITMSPSAVLMHVEKEKYVRLNSQK 202  
 Query 197 SVPLYSCEAWPEKGMREVVTVLPSHIYLAFLALIVMYARIARKLCAQAPGAPGGEA 256  
 + P+Y C E WP + MR++YTVLF++IYLAFL+LIV+MY RI L+ A P G +  
 Sbjct 203 TSPVYWCREDWPNQENRKIIYTVLFANITYLAFLSLIVIMYGRIGISLFAAVPHTRKQK 262  
 Query 257 ADPR-ASRRARVVMHMLVQALFTSLNPLWALLLLIDYQGLSAPQLHVTYVPPFAH 315  
 SR++ +++ ML++VAL F LSNLPLM L++L DY LS -L++ +Y +PPFAH  
 Sbjct 263 EQWVVSRKKQIKIMLLIVALLFISLWPLWTLMLSDYADLSFHEQLIINIYVPPFAH 322  
 Query 316 WLAFNSSANPIIYGFNFNFRGQFAAFARLCPRPSGSHKEAYSER 363  
 WLAF NSS NPIIYG-FNFNFRGQ AF+ +LC + + EAY+ +  
 Sbjct 323 WLAFGSSVNPIIYGFNFNFRGQFAAFQQLQCKRAKP-MEAYALK 366

>gb|AAK58513.1|AF236083\_1 [C] G-protein-coupled receptor 74 [Homo sapiens]  
 Length=408

GENE ID: 10886 NPFRF2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 422 bits (1084), Expect = 2e-117, Method: Compositional matrix adjust.  
 Identities = 197/348 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)  
 Query 18 NGTNTTEATPATNLTFSSYQHTSPVAAMFIVAYAILFLCKMGNTLVCFVLKRNHMTV 77  
 N T N+T+ +Y H VAA-FI++Y LIF LCM-GNT+VCFIV++N+HMTV  
 Sbjct 23 NDTKHLHLYSDINITYVNYLHQVQAAIFIIISYFLFLCKMGNTVVCFIVMRKNHMTV 82  
 Query 78 TNMFLINLAUSDLLGIFCMPTTLVDMLITGWPFNDKATCMGSLVQGMVSASVFTLVAI 137  
 TN+FLINLA+SDLLGIFCMPT TL+DN+I GWPF N CK+SLGVQ+SV+ASVFTLVAI  
 Sbjct 83 TNLFLINLAISDLLGIFCMPTILLDNIAGWPFNTCKISGLVQGISVAASVFTLVAI 142  
 Query 138 AVFRFCIVHPFPEKLTIRKALVTIAVWALALLIMCPSAVLTITVREEHFM-VDARRN 196  
 AV+RF+C+V+PF+ KLT++ A V I +W LA+ IM PSV L V E+++ + +++N+  
 Sbjct 143 AVDRFCQVVPFPEKLTITKTAFTVIMIIWVLAITMSPSAVLMHVEKEKYVRLNSQK 202  
 Query 197 SVPLYSCEAWPEKGMREVVTVLPSHIYLAFLALIVMYARIARKLCAQAPGAPGGEA 256  
 + P+Y C E WP + MR++YTVLF++IYLAFL+LIV+MY RI L+ A P G +  
 Sbjct 203 TSPVYWCREDWPNQENRKIIYTVLFANITYLAFLSLIVIMYGRIGISLFAAVPHTRKQK 262  
 Query 257 ADPR-ASRRARVVMHMLVQALFTSLNPLWALLLLIDYQGLSAPQLHVTYVPPFAH 315  
 SR++ +++ ML++VAL F LSNLPLM L++L DY LS -L++ +Y +PPFAH  
 Sbjct 263 EQWVVSRKKQIKIMLLIVALLFISLWPLWTLMLSDYADLSFHEQLIINIYVPPFAH 322  
 Query 316 WLAFNSSANPIIYGFNFNFRGQFAAFARLCPRPSGSHKEAYSER 363  
 WLAF NSS NPIIYG-FNFNFRGQ AF+ +LC + + EAY+ +  
 Sbjct 323 WLAFGSSVNPIIYGFNFNFRGQFAAFQQLQCKRAKP-MEAYALK 366

>gb|AAD22047.1| [C] G-protein-coupled receptor [Homo sapiens]  
 Length=522

GENE ID: 10886 NPFRF2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 420 bits (1080), Expect = 4e-117, Method: Compositional matrix adjust.  
 Identities = 197/346 (56%), Positives = 264/346 (76%), Gaps = 3/346 (0%)  
 Query 18 NGTNTTEATPATNLTFSSYQHTSPVAAMFIVAYAILFLCKMGNTLVCFVLKRNHMTV 77  
 N T N+T+ +Y H VAA-FI++Y LIF LCM-GNT+VCFIV++N+HMTV  
 Sbjct 122 NDTKHLHLYSDINITYVNYLHQVQAAIFIIISYFLFLCKMGNTVVCFIVMRKNHMTV 181  
 Query 78 TNMFLINLAUSDLLGIFCMPTTLVDMLITGWPFNDKATCMGSLVQGMVSASVFTLVAI 137  
 TN+FLINLA+SDLLGIFCMPT TL+DN+I GWPF N CK+SLGVQ+SV+ASVFTLVAI  
 Sbjct 181 TNLFLINLAISDLLGIFCMPTILLDNIAGWPFNTCKISGLVQGISVAASVFTLVAI 241  
 Query 138 AVFRFCIVHPFPEKLTIRKALVTIAVWALALLIMCPSAVLTITVREEHFM-VDARRN 196  
 AV+RF+C+V+PF+ KLT++ A V I +W LA+ IM PSV L V E+++ + +++N+  
 Sbjct 242 AVDRFCQVVPFPEKLTITKTAFTVIMIIWVLAITMSPSAVLMHVEKEKYVRLNSQK 301  
 Query 197 SVPLYSCEAWPEKGMREVVTVLPSHIYLAFLALIVMYARIARKLCAQAPGAPGGEA 256  
 + P+Y C E WP + MR++YTVLF++IYLAFL+LIV+MY RI L+ A P G +  
 Sbjct 302 TSPVYWCREDWPNQENRKIIYTVLFANITYLAFLSLIVIMYGRIGISLFAAVPHTRKQK 361  
 Query 257 ADPR-ASRRARVVMHMLVQALFTSLNPLWALLLLIDYQGLSAPQLHVTYVPPFAH 315  
 SR++ +++ ML++VAL F LSNLPLM L++L DY LS -L++ +Y +PPFAH  
 Sbjct 362 EQWVVSRKKQIKIMLLIVALLFISLWPLWTLMLSDYADLSFHEQLIINIYVPPFAH 421  
 Query 316 WLAFNSSANPIIYGFNFNFRGQFAAFARLCPRPSGSHKEAYS 361  
 WLAF NSS NPIIYG-FNFNFRGQ AF+ +LC + + EAY+ +  
 Sbjct 422 WLAFGSSVNPIIYGFNFNFRGQFAAFQQLQCKRAKP-MEAYT 466

>ref|NP\_004876.2| [C] neuropeptide FF receptor 2 isoform 1 [Homo sapiens]  
 sp|Q9T5X5.2|NPFF2\_HUMAN [C] RecName: Full=Neuropeptide FF receptor 2; AltName: Full=Neuropeptide G-protein coupled receptor; AltName: Full=G-protein coupled receptor 74; AltName: Full=G-protein coupled receptor  
 R04877

gb|XAX05649.1| [C] neuropeptide FF receptor 2, isoform CRA\_c [Homo sapiens]  
 Length=522

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 420 bits (1080), Expect = 4e-117, Method: Compositional matrix adjust.  
 Identities = 197/346 (56%), Positives = 264/346 (76%), Gaps = 3/346 (0%)

Query 18 NGTNEATPATNLTFSSYQHTSPVAMFIVAYALIFLLCMVGNLTVCVFLVKNRHHGTV 77  
 N T N+T+ +Y H VAA+Fi+Y LIF LCM+GNT+VCFIV+ +N+HHGTV  
 Sbjct 122 NDTXHHLSIDNITVYVNLHQVQVAIFIIISYFLIFLLCMGNTVVCVFLVNRKHHGTV 181

Query 78 TMTFILNALVDLVLGIFCMPTTLVDNLITGMFPFNATCMKSLGVQMSVSASVPTLVAI 137  
 TM+FILNA+SDLVGIPTCP TL+DNI GMFF N C+ SGLVQMSV+ASVPTLVAI  
 Sbjct 182 TNLFILNALISDLVGIPTCPITLLDNIAGWPFNTCMKISGLVQMSVSAASVPTLVAI 241

Query 138 AVERPRCIVHPFREKLTLKALVTIAVIMALLIMCPSAVTLTITREEHHFM+VDARNR 196  
 AV+RF+C+V+PF+ KLT++ A V I +M LA+ IM PSV L V B++ + ++N+  
 Sbjct 242 AVDRFQCVYVFPFKLTITKTAFTVIMILVLAITIMSPSAVMLHVQEKRYVRLNSQK 301

Query 197 SYPLYSCEWAEPEKGMREYVTTVLFSHIYLAFLALIVVMYARIKLCQAPGAPGREA 256  
 P+Y C E NP + MR +YTTVL++IYLAFL+LIV+MY RI L +A P G +  
 Sbjct 302 TSPVYRCRWPNQKRSITITVLFAMILAF+LIVMYRIGISLAPRAAVPHYGRKQ 361

Query 257 ADPR+ASRRARRVVMILVAFPT+SNPLAALLIDYQLSAPQLHLVTPYAPFAN 315  
 SR++ ++ ML++VAL F LSWLPLW L++L Y LS +L ++ +Y +PFAH  
 Sbjct 362 EQHVRVSRKKQIKMKLLIALLFVLSWLPWLTLMLSLDYADLSPLNELQINITYPPAH 421

Query 316 WLAFPNSSANFIYGYFNNFRPGQPAAPRRLCPRPGSHKEAYS 361  
 WLAF NSS NPITYG+PNNFRPGQ AP+ +LC + + EAY+  
 Sbjct 422 WLAFPNSSVNPITYGPNFRPGQPAAPQLCQKRAK+MEAYA 466

>gb|XAX05647.1| [C] neuropeptide FF receptor 2, isoform CRA\_a [Homo sapiens]  
 Length=304

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 286 bits (732), Expect = 1e-76, Method: Compositional matrix adjust.  
 Identities = 135/248 (54%), Positives = 186/248 (75%), Gaps = 3/248 (1%)

Query 116 CMSGSLVQMSVSASVPTLVAIAVERPRCIVHPFREKLTLKALVTIAVIMALLIMCP 175  
 CK+SGLVQ+SV+ASVPTLVAIAIAV+RF+C+V+PF+ KLT++ A V I +M LA+ IM P  
 Sbjct 2 C KISGLVQMSVSAASVPTLVAIAVDRFQCVYVFPFKLTITKTAFTVIMILVLAITIMSP 61

Query 176 SAVTLTITREEHHFM+VDARNRSYPLYSCEWAEPEKGMREYVTTVLFSHIYLAFLALIV 234  
 SAV L V B++ + ++N++ P+Y C E NP + MR +YTTVL++IYLAFL+LIV+  
 Sbjct 62 SAVLHVGRKRYVTVLNSKQMSPTVTCRHWQKMKITTVTLFANILAPLSLIV 121

Query 235 MYARIARKLCQAPGAPGGEAADPRA+SRRRARRVVMILVAFPT+SNPLAALLIDYQLS 293  
 MY RI L +A P G + SR++ ++ ML++VAL F LSWLPLW L++L Y  
 Sbjct 122 MYRIGISLAPRAAVPHYGRKQKQVHVRVSRKKQIKMKLLIALLFVLSWLPWLTLMLSL 181

Query 294 DYQQLSAPQLHLVTPYAPFANHLAFNNSANFIYGYFNNFRPGQPAAPRRLCPRS 353  
 DY LS +L ++ +Y +PFAHWLAF NSS NPITYG+PNNFRPGQ AP+ +LC +  
 Sbjct 182 DYADLSPLNELQINITYPPAHWLAFNNSVNPITYGPNFRPGQPAAPQLCQK+R 240

Query 354 GSHKEAYS 361  
 EAY+  
 Sbjct 241 AKMPEAYA 248

>ref|NP\_001517.2| [C] orexin receptor 2 [Homo sapiens]  
 sp|Q43614.2|OX2R\_HUMAN [C] RecName: Full=Orexin receptor type 2; AltName: Full=Ox2r; AltName: Full=Hypocretin receptor type 2  
 emb|CAR73407.1| [C] hypocretin (orexin) receptor 2 [Homo sapiens]  
 emb|CAI19665.1| [C] hypocretin (orexin) receptor 2 [Homo sapiens]  
 gb|XAX04440.1| [C] hypocretin (orexin) receptor 2 [Homo sapiens]  
 Length=444

GENE ID: 3062 HCRT2 | hypocretin (orexin) receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 190 bits (483), Expect = 7e-48, Method: Compositional matrix adjust.  
 Identities = 128/376 (34%), Positives = 189/376 (50%), Gaps = 41/376 (10%)

Query 6 SOPPNSWFLSQNGTNEA-----TPATNLTFSSY----YQHTSPVAMFIVAYALIFLL 56  
 PP LN + T+ T+ + F Y Y H + + I Y ++P++  
 Sbjct 8 DSPCKRRMSASELNFQETPLPTDYDEDFLRVILMREYLPKEWVLGATYIVVW 67

Query 57 CMVGNLTVCVFLVKNRHHGTVTMTFILNALVDLVLGIFCMPTTLVDNLITGMFPFNAT 116  
 +CM LNC V GN IVM TTM FI+H++D+LV I C+P TLV + + N P + C  
 Sbjct 68 ALIGNMLVLCVAVNHHHMTVINYFIWLSLADLVITITCLPATIVVDITFTWFGQSLC 127

Query 117 KMSGSLVQMSVSASVPTLVAIAVERPRCIVHPFREKLTLKALVTIAVIMALLIMCPS 176  
 K+ +Q +SVS SV TL IA+R+ I HP K T ++A +I +M ++ +IM P  
 Sbjct 128 KVPIPLTVSVSVLTLSCIALDRMYAICHPMFKSTAKKARMSVIVIWISCIIMIPQ 187

Query 177 AVTLTITREEHHFMVDARNRSYPLYSCEWAEPEKGMREYVTTVLFSHIYLAFLALIVMY 236  
 R+ +E LNC V GN IVM TTM FI+H++D+LV I C+P TLV + + N P + C  
 Sbjct 188 AITVM-----ECSTVPGLANKTITVTCDSRMGGEIYFPMYHICFLLVTVAPLCMLVAY 243

Query 237 ARIARKC-C-QAPGPA-----PG-----GEEAADPRASRRARRV 269  
 +I KKI C Q PG + PG AA+ + R R +  
 Sbjct 244 LQIFRKLRCRQIPGTSVVQRKWLQPVQSPRGPGQPTKSRMSAAAEIKQIRARRKTA 303



Query 270 HMLVVALFPTLSWLPALLLLIDYQSLAPQLHLVTVA-PPFAHMLAFNSSANPII 328  
ML+V L F + +LP+ L +L + A TVYA F P+HML + NS+ANPII  
Sbjct 304 RMLMIVLLFAICYLIPISILNVLKRVFGMPANTDETRTYAMFTPSHVLVANSANPII 363

Query 329 GYFNENFRFGQAAF 344  
Y + FR F+AAF  
Sbjct 364 YNPLSGKFRFEEKAAF 379

>gb|AAC39602.1| **G** orexin receptor-2; OX2R; G protein-coupled receptor [Homo sapiens]  
>AAC28021.1| **G** hypocretin receptor-2 [Homo sapiens]  
gb|AAL47215.1| **G** hypocretin receptor 2; orexin receptor 2 [Homo sapiens]  
dbj|BAK6939.1| **G** unnamed protein product [Homo sapiens]  
Length=444

GENE ID: 3062 HCRTR2 | hypocretin (orexin) receptor 2 [Homo sapiens]  
(Over 10 PubMed links)  
Score = 190 bits (483), Expect = 7e-48, Method: Compositional matrix adjust.  
Identities = 128/376 (34%), Positives = 189/376 (50%), Gaps = 41/376 (10%)

Query 6 SQPNSSNPLSQNGINTA-----TPATMLTFSSY---YQTSFVAMFIVAYALIFLL 56  
PP +H + T + F Y YH + I Y ++F+  
Sbjct 8 DSSPCNSSASSELNETQEPFLNPTDYDEEFLAYLMREYHFKREYENVLGIIVFV 67

Query 57 CMVGTLCVPIVLRNHRMTVTNMFILNVLAVSLDGLGFCMPTTLVNLITGWFPDNATCKMS 116  
+GN LVC V KN HK TVTN FI+NL+++D+LV I C+P TLV ++ W F + C  
Sbjct 68 ALIGKLVLRNHRMTVTNMFILNVLAVSLDGLGFCMPTTLVNLITGWFPDNATCKMS 126

Query 117 EMSGVQGSVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAVIALALLMCPSS 176  
K +O S+VS SV TI ID++R+ I HP K T +A +I +W ++ +W P  
Sbjct 128 KVIPIYLTQVSVSVLTLSPALDRWYACHPLFKSTAKKARSIVIIWISCIIMIPQ 187

Query 177 AVTLVTRREHHFMDARNRSGYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLIVVMY 236  
A + E N+ C E W + ++Y F Y+APL L+V+ Y  
Sbjct 188 AIVM----ECSTVFPGLNKTTLFTVCDERNGGIEIYPMYHICFFLVTNAPLCLNVLAY 243

Query 237 ARIARKC-C-QAPGPA-----DG-----GEEAADPRASRRARVV 269  
+I RKL C PG +G A+ + R R  
Sbjct 244 LQIFRKLWCRQIPGTSSVQQRKWKPLQVSPQPGQPTSKRMSVAVAEIKQIRARAKTA 303

Query 270 HMLVVALFPTLSWLPALLLLIDYQSLAPQLHLVTVA-PPFAHMLAFNSSANPII 328  
ML+V L F + +LP+ L +L + A TVYA F P+HML + NS+ANPII  
Sbjct 304 RMLMIVLLFAICYLIPISILNVLKRVFGMPANTDETRTYAMFTPSHVLVANSANPII 363

Query 329 GYFNENFRFGQAAF 344  
Y + FR F+AAF  
Sbjct 364 YNPLSGKFRFEEKAAF 379

>gb|AAC39601.1| **G** orexin receptor-1; OX1R; G protein-coupled receptor [Homo sapiens]  
Length=425

GENE ID: 3061 HCRTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]  
(Over 10 PubMed links)  
Score = 181 bits (459), Expect = 4e-45, Method: Compositional matrix adjust.  
Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

Query 60 GNTLVCFIVLRNHRMTVTNMFILNVLAVSLDGLGFCMPTTLVNLITGWFPDNATCKMS 119  
GNTLVC V +N HM TVTN FI+NL+++D+LV C+P L+ ++ W F +A CK+  
Sbjct 63 GNTLVCLAVRNHRMTVTNMFILNVLAVSLDGLGFCMPTTLVNLITGWFPDNATCKMS 122

Query 120 GLVQGSVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAVIALALLMCPSSAVT 179  
+O +SVS +V TL ID++R+ I HP K T R+A +I ID++L IM P A  
Sbjct 123 PYLQAVSVSAVLTLSFALDRWYACHPLFKSTAKKARSIVIIWISCIIMIPQ 182

Query 180 LTVTRREHHFMDARNRSGYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLIVVMYARI 239  
+ E + + NR+ C E W + ++Y F Y+APL L+V+ Y +I  
Sbjct 183 M----ECSSVLPELANRTRLSVCDERNADDLVYKTHSCFPIYTVLAFLQINAMAYPT 238

Query 240 ARKLC-QAPG-----DG-----PAPOGER-AADPRASRRARVVH 270  
RKL C PG +G A+ + R R  
Sbjct 239 PRKMLWCRQIPGTSSVQQRKWKPLQVSPQPGQPTSKRMSVAVAEIKQIRARAKTA 298

Query 271 HMLVVALFPTLSWLPALLLLIDYQSLAPQLHLVTVA-PPFAHMLAFNSSANPII 329  
ML+V L F +LP+ L +L + A TVYA F P+HML + NS+ANPII  
Sbjct 299 RMLMIVLLFAICYLIPISILNVLKRVFGMPANTDETRTYAMFTPSHVLVANSANPII 358

Query 330 GYFNENFRFGQAAF 344  
Y + FR F+AAF  
Sbjct 359 YNPLSGKFRFEEKAAF 379

>ref|NP\_001516.2| **G** orexin receptor 1 [Homo sapiens]  
sp|Q43613.2|OX1R\_HUMAN **G** RecName: Full=Orexin receptor type 1; AltName: Full=Ox1r; AltName: Full=Hypocretin receptor type 1  
gb|AA028020.1| **G** hypocretin receptor-1 [Homo sapiens]  
gb|AAL47214.1| **G** hypocretin receptor 1; orexin receptor 1 [Homo sapiens]  
gb|AAL50221.1| **G** hypocretin receptor 1 [Homo sapiens]  
gb|AAH74796.1| **G** Hypocretin (orexin) receptor 1 [Homo sapiens]  
gb|KAX07602.1| **G** hypocretin (orexin) receptor 1, isoform CRA\_c [Homo sapiens]  
Length=425

GENE ID: 3061 HCRTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]  
(Over 10 PubMed links)  
Score = 179 bits (453), Expect = 2e-44, Method: Compositional matrix adjust.  
Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

Query 60 GNTLVCFIVLRNHRMTVTNMFILNVLAVSLDGLGFCMPTTLVNLITGWFPDNATCKMS 119

Sbjct 63 GNTLWC V +N HM TVTN FI+NL++D+LV C+P +L+ + W P +A CK- 122  
GNTLVCLAVNRNHHMRTVNTFYIWNLSLADVLTAICLPSALLVDITESNLGHALCKVI

Query 120 GLVQGVSVASVFTLVIAIAVERFCIVHPFREKLTLKALVTIAVIMWALALLMCPASVT 179  
+Q +SVS +V TL IA++R+ I HP K T R+A +I IWA++L IM P A

Sbjct 123 PYLQGVSVASVFTLVIAIAVERFCIVHPFREKLTLKALVTIAVIMWALALLMCPASVT 182  
+Q +SVS +V TL IA++R+ I HP K T R+A +I IWA++L IM P A

Query 180 LTVTREETHHFMVDARNRSPYLYSCHEAWPEKGMRRVYTVLFSHIYLAFLALIVVMYARI 239  
+ E + + NR+ C E W + ++Y + F YLAPL L+ + Y +I

Sbjct 183 M----ECSVSLVELANRTRLSVCDERADDLYPKIYHSCFFIYTVLAPLGLAMAYPTOI 238

Query 240 ARKLC -QAQGPAPG-----GEEAAD-----PRAS-----RRRARVHH 270  
REL Q PG ++ D PRA R R +

Sbjct 239 FRKLWGQIGPTTSALVRNWRKPSDQGLDLEQGLSGEPQPRARAFLEAVKQMRARRKTAK 298

Query 271 MLNVAVFLPFLSNLWALLLLIDYGLSAPQLHLVTVYA-PPFAHFLAFFNSSANPIIY 329  
ML++V L F L +L+ L +L + VTA F F+HML + NS+ANPIIY

Sbjct 299 MLNVLVLVFLCYLPSVNLVLRKVPGRQASDREAVYACFTFSHMLVYANSAANPIIY 358

Query 330 GYPNENFRGQQAAPRRL-----CPRPSGSHKE 358  
+ + FR P+AP L PR S SHK

Sbjct 359 NFLSGKFRDQKAAPSCCLPGGLPGSLKAPSPRSSASHKS 399

>dbj|BAF83210.1| **G** unnamed protein product [Homo sapiens]  
Length=425

GENE ID: 3661 HCRTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 179 bits (453), Expect = 2e-44, Method: Compositional matrix adjust.  
Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

Query 60 GNTLWC V +N HM TVTN FI+NL++D+LV C+P +L+ + W P +A CK- 119  
GNTLVCLAVNRNHHMRTVNTFYIWNLSLADVLTAICLPSALLVDITESNLGHALCKVI

Sbjct 63 GNTLVCLAVNRNHHMRTVNTFYIWNLSLADVLTAICLPSALLVDITESNLGHALCKVI 122

Query 120 GLVQGVSVASVFTLVIAIAVERFCIVHPFREKLTLKALVTIAVIMWALALLMCPASVT 179  
+Q +SVS +V TL IA++R+ I HP K T R+A +I IWA++L IM P A

Sbjct 123 PYLQGVSVASVFTLVIAIAVERFCIVHPFREKLTLKALVTIAVIMWALALLMCPASVT 182  
+Q +SVS +V TL IA++R+ I HP K T R+A +I IWA++L IM P A

Query 180 LTVTREETHHFMVDARNRSPYLYSCHEAWPEKGMRRVYTVLFSHIYLAFLALIVVMYARI 239  
+ E + + NR+ C E W + ++Y + F YLAPL L+ + Y +I

Sbjct 183 M----ECSVSLVELANRTRLSVCDERADDLYPKIYHSCFFIYTVLAPLGLAMAYPTOI 238

Query 240 ARKLC -QAQGPAPG-----GEEAAD-----PRAS-----RRRARVHH 270  
REL Q PG ++ D PRA R R +

Sbjct 239 FRKLWGQIGPTTSALVRNWRKPSDQGLDLEQGLSGEPQPRARAFLEAVKQMRARRKTAK 298

Query 271 MLNVAVFLPFLSNLWALLLLIDYGLSAPQLHLVTVYA-PPFAHFLAFFNSSANPIIY 329  
ML++V L F L +L+ L +L + VTA F F+HML + NS+ANPIIY

Sbjct 299 MLNVLVLVFLCYLPSVNLVLRKVPGRQASDREAVYACFTFSHMLVYANSAANPIIY 358

Query 330 GYPNENFRGQQAAPRRL-----CPRPSGSHKE 358  
+ + FR P+AP L PR S SHK

Sbjct 359 NFLSGKFRDQKAAPSCCLPGGLPGSLKAPSPRSSASHKS 399

>ref|NP\_000901.1| **G** neurotensin Y receptor Y2 [Homo sapiens]  
sp|P49146.1|NPY2R\_HUMAN **G** RecName: Full=Neurotensin Y receptor type 2; Short=NPY2R; AltName:  
Full=NPY2 receptor; Short=Y2 receptor

gb|AAC50281.1| **G** neurotensin Y/peptide YY Y2 receptor

gb|AAB04120.1| **G** neurotensin Y2 receptor

gb|AAC51115.1| **G** type 2 neurotensin Y receptor

gb|AAO92062.1| **G** neurotensin Y receptor Y2 [Homo sapiens]

gb|AAH75052.2| **G** Neurotensin Y receptor Y2 [Homo sapiens]

gb|AAH75053.2| **G** Neurotensin Y receptor Y2 [Homo sapiens]

gb|AAI40940.1| **G** unknown [Homo sapiens]

gb|EAX04901.1| **G** neurotensin Y receptor Y2 [Homo sapiens]  
Length=381

GENE ID: 4887 NPY2R | neurotensin Y receptor Y2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 167 bits (422), Expect = 9e-41, Method: Compositional matrix adjust.  
Identities = 112/322 (34%), Positives = 164/322 (50%), Gaps = 23/322 (7%)

Query 42 VAAPIVAVYALIFLLCGVNTLVCFIVLDRHMTVNTFNLNLAWSLDLVIGIFCPMPTL 101  
V + I L Y + I L + +GN+LV +V+K + M TVTN FI NEAV+DLV C+P TL

Sbjct 49 VQVVLILAYCSIIILGVIGNSLVIRHVIFKFSMTVNTFNLNLAWSLDLVIGIFCPMPTL 108

Query 102 VDNLTGWPFNATACIOMGLVQGVSVASVFTLVIAIAVERFCIVHPFREKLTLKALVT 161  
L+ W C + QG++V S TL IA++R RCIV+ K+ R + +

Sbjct 109 TTYLGEWKGWGFVLCVLPVYQGLAVGVSTITLVIALDRHRCIVTHLESKIKRISFLI 168

Query 162 IAVNALALLMCPASVTLTVTREETHHFMVDARNRSPYLYSCHEAWPE- EKGMR- RYVTT 218  
I + W ++ L P L + RE + + + + C E WP EK + VY+

Sbjct 169 IGLAWKISALLASP-----IAIFPYSLETIIP---DFEIVACTEKWREKSTIYTVYSIL 221

Query 219 VLFSHIYLAFLALIVVMYARIKRLQAQGPAPGGEAADPRASRRARVHHMLNVAFL 278  
+Y+ PL + I Y RI KL P AA+ +RR+ + MLV V +

Sbjct 222 SSSLILVLPGLIGISYSTRITWSLKHVSPG-----AANDHYHRRQKTKMLVCVVV 276

Query 279 FTLSNLPLNALLLLIDYGL-LSAPQLHLVTVYAFPAHFLAFFNSSANPIIYGYPNENF 336  
F +SNLPL A L +D L +L + F R H A + + ANP++YG+ N N+

Sbjct 277 FAVSNLPLNALLLLIDYGLVQLDLYKGLI-----FTVFIIAMCTSFANFLWGMNSY 332

Query 337 RRGQAAPRRLCPRPSGSHKE 358  
R+ P +APR R H E

Sbjct 333 RKAFSAFRCE--QRDLATHSE 352

>gb|AAA93170.1| **G** type 2 neuropeptide Y receptor  
Length=381

GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 165 bits (417), Expect = 3e-40, Method: Compositional matrix adjust.  
Identities = 113/322 (34%), Positives = 163/322 (50%), Gaps = 23/322 (7%)

Query 42 VAMFIVAYALFLPCLVGNLTLCFVILNKRHMVITVNMFLINLAVALDGLVIFPCMTPTL 101  
V L I T Y I L L + G H I V + Y R + M T V N F I M L A V S D L L V I F C P T L  
Sbjct 49 VQVVLILAYCSIIHLGVISNLSIVIRVIFKPSMRTVTFPIANLAVADLLNLTCLPPTL 108

Query 102 VDNLTGWPFDNATCKMSGLVQMSVSFVTLVAIAVERFCIVHPFEKLTLRKALVT 161  
L + W C + QG+ S T L I A + R R C I V + K + R + +  
Sbjct 109 TTTIGGEWKNQPVLCILVFPVQGLAAQVSTITLTVALDHRHCITVHLESIKSRISFL 168

Query 162 IAVINALALLINCPASVTLTVTREHHFPMVDARNRSTPLYSCEWAPN - EKGR - RVYIT 218  
I + + + L L + L + R E + + + C E W P E K + + V Y I  
Sbjct 169 IGLANGSALLASP - - - LAITREYSILIEIP - - - DFEIVATCKQNRGRSIVGYTVEL 221

Query 219 VLFSHIYIAPLALIVMYIARLKCQAPQAGEEADPRASRRRARVVMVLVWALF 278  
Y + P L + I Y R I K L P A A + + R R + M L V + +  
Sbjct 222 SLLILIVLPLGLIISPSYTRISWKLKHVSPG - - - AANDHYHOROKTTKMLVCVVV 276

Query 279 FTLNWLPLWALLLLIDYQ - - LSAPQLHLVTYAFPAHNLAFNSSANPIIYGYNENF 336  
P + SWLPL A L D L + L + P H A + + ANP + YG + N N +  
Sbjct 277 FAVSNLPLHAPQLAVIDBSQVLDLKEYLI - - - FTVPHIIMCSTTANFLVGMNENY 332

Query 337 RRGPAAPFARLCPRSGSHKE 358  
R + P AFR R H E  
Sbjct 333 RKAFLSAFRCE - - ORLDIHRS 352

>ref|NP\_937822.2| **G** G protein-coupled receptor 103 [Homo sapiens]  
gi|95665.2|ORFPR\_HUMAN **G** RecName: Full=Orexigenic neuropeptide ORFP receptor; AltName: Full=G-protein coupled receptor 103; AltName: Full=SP9155; AltName: Full=AO27  
gb|EAX05262.1| **G** G protein-coupled receptor 103, isoform CRA\_b [Homo sapiens]  
Length=431

GENE ID: 84109 ORFPR | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer PubMed links)

Score = 165 bits (417), Expect = 3e-40, Method: Compositional matrix adjust.  
Identities = 93/304 (30%), Positives = 159/304 (52%), Gaps = 21/304 (6%)

Query 51 ALIFLCLVGNLTLCFVILNKRHMVITVNMFLINLAVALDGLVIFPCMTPTLVNLTGW 110  
L I F L + G N I V + V + + M T V N + F I + L A + S D L L + F C + P T + N + W  
Sbjct 53 VLIFALALPINALVFPVTVTSKAMRTVTNIFICSLASDLLITFFCIPVTMLQINISNLL 112

Query 111 FDNATCKMSGLVQMSVSFVTLVAIAVERFCIVHPFEK - LTLRKALVTIAVIAL 168  
CKM VQ + V + T + I A V E R + + V H P + K T R A + + V + W +  
Sbjct 113 GGAFICKMPVFQSTAVTVTEILTNTCIAVERHQGLVHPFKMKQVYTRNAPATMLGVMLV 172

Query 169 ALLINCP - SAVTLTVTREHHFPMVDARNRSTPLYSCEWAPNPKGRMRVTVTLFHSIYL 226  
+ P L + P L + + P E + + C E W + + Y T I + + L  
Sbjct 173 AVIVSGPMWVHQQLEI - - KYDFLYEKH - - - ICCLEWTSVPVHOKITVTPILVILFL 224

Query 227 APALIVMYIARLKCQAPQAPG - - - - - GEEADPRASRRRARVVMVLVWALFP 279  
P L + + + + Y + I + L G G E + + + R + + R V M + V P F  
Sbjct 225 LPLMVLILYSIKIGELAIKKRVGGSGVLRTINGKMS - KIARKKKRAVIMVTVVVALP 282

Query 280 TLSWLPLWALLLLIDYGLSAPQLHLVTYAFPAHNLAFNSSANPIIYGYNENFRG 339  
+ N P + + + I Y + + + P + P N S N P I Y + N E N F +  
Sbjct 283 AVCNAPFHVVMHIEYSNFEKEDYDTIKMIFAIQVIGFNSICNPITYVAPNENFKN 342

Query 340 PQAA 343  
+ A  
Sbjct 343 VLSA 346

>dbj|BAC98938.1| **G** ORFP receptor [Homo sapiens]  
Length=431

GENE ID: 84109 ORFPR | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer PubMed links)

Score = 164 bits (416), Expect = 6e-40, Method: Compositional matrix adjust.  
Identities = 93/304 (30%), Positives = 159/304 (52%), Gaps = 21/304 (6%)

Query 51 ALIFLCLVGNLTLCFVILNKRHMVITVNMFLINLAVALDGLVIFPCMTPTLVNLTGW 110  
L I F L + G N I V + V + + M T V N + F I + L A + S D L L + F C + P T + N + W  
Sbjct 53 VLIFALALPINALVFPVTVTSKAMRTVTNIFICSLASDLLITFFCIPVTMLQINISNLL 112

Query 111 FDNATCKMSGLVQMSVSFVTLVAIAVERFCIVHPFEK - LTLRKALVTIAVIAL 168  
CKM VQ + V + T + I A V E R + + V H P + K T R A + + V + W +  
Sbjct 113 GGAFICKMPVFQSTAVTVTEILTNTCIAVERHQGLVHPFKMKQVYTRNAPATMLGVMLV 172

Query 169 ALLINCP - SAVTLTVTREHHFPMVDARNRSTPLYSCEWAPNPKGRMRVTVTLFHSIYL 226  
+ P L + P L + + P E + + C E W + + Y T I + + L  
Sbjct 173 AVIVSGPMWVHQQLEI - - KYDFLYEKH - - - ICCLEWTSVPVHOKITVTPILVILFL 224

Query 227 APALIVMYIARLKCQAPQAPG - - - - - GEEADPRASRRRARVVMVLVWALFP 279  
P L + + + + Y + I + L G G E + + + R + + R V M + V P F  
Sbjct 225 LPLMVLILYSIKIGELAIKKRVGGSGVLRTINGKMS - KIARKKKRAVIMVTVVVALP 282

Query 280 TLSWLPLWALLLLIDYGLSAPQLHLVTYAFPAHNLAFNSSANPIIYGYNENFRG 339  
+ N P + + + I Y + + + P + P N S N P I Y + N E N F +  
Sbjct 283 AVCNAPFHVVMHIEYSNFEKEDYDTIKMIFAIQVIGFNSICNPITYVAPNENFKN 342

Query 340 PQAA 343  
+ A  
Sbjct 343 VLSA 346

>gb|AAD00248.1| **C** neuropeptide Y receptor type 2 [Homo sapiens]  
 Length=381  
 GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 164 bits (416), Expect = 5e-40, Method: Compositional matrix adjust.  
 Identities = 111/322 (34%), Positives = 164/322 (50%), Gaps = 23/322 (7%)  
 Query 42 VAAVFVAVAIIFLLCVGNLTLCVFLVKNRHMRTVTNMFILNLAVSLDLGIFCMPTTL 101  
 V + L+Y I LL ++GM+LV ++K + M TVTN FI NLAV+DLV C+P TL  
 Sbjct 49 VQVVLILAYCSITLLGVIGNSLVIRHVIFKFSMRTVTNFFIANLAVADLLVNTLCPLPTL 108  
 Query 102 VNDLITGMFPFNATCKMSGLVQGMVSASVFTLVAIAVERFCIVHFFPREKLIRKALVT 161  
 L+ M C + QG+V S TL IR+R RCIV K+ R + +  
 Sbjct 109 TTYLGMGKMGVFLCHLVPAQGLAVGVSTITLTVIALDRHRCIVYHLESKISKRISFLI 166  
 Query 162 IAVIALALLIMCPSAVTLTVTREHHFMDARNRSPYLYSCWAMP--EKGR-RVYT 218  
 I + M ++L+ P L + RE ++ + + C E WP EK + VY+  
 Sbjct 169 IGLAMGISALLASP---LAIFREYSLIEIIP---DFEIVACTEWPGEERKISYGVYSEL 221  
 Query 219 VLFSHIYALPLALIVVMYARIARLCOAPGAPGAGEAADPRASRRRARVVMHVAWVAF 278  
 Y+ PL +I Y RI KL P A+ ++RR + MLV Y +  
 Sbjct 222 SLLILTVPLIGIISFSYTRINSLKSHVSPG-----AANDHYQRORQRTIMLCVGVVV 276  
 Query 279 FTLSNLPALWALLLLIDYQG--LSAPQLHLTVYAPFAHNLAFPNSSANPIIYGVFNENF 336  
 F +SNLPL A L +D L + L+ P +A ++ANP++YG+ N N+  
 Sbjct 277 FAVSWPLHAFQLAVIDDSQVLDLKEYLKI---FTVFHIIAMCTIFANFLYGVNNSNY 332  
 Query 337 RRGFOAARFARLCRPSGSKE 358  
 R+ F +FR R H R  
 Sbjct 333 RKAFLSAFRCE--QRDLAIRSE 352

>gb|AAB07760.1| **C** neuropeptide y/peptide YY receptor type 2  
 Length=381  
 GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 164 bits (414), Expect = 6e-40, Method: Compositional matrix adjust.  
 Identities = 112/322 (34%), Positives = 163/322 (50%), Gaps = 23/322 (7%)  
 Query 42 VAAVFVAVAIIFLLCVGNLTLCVFLVKNRHMRTVTNMFILNLAVSLDLGIFCMPTTL 101  
 V + L+Y I LL ++GM+LV ++K + M TVTN FI NLAV+DLV C+P TL  
 Sbjct 49 VQVVLILAYCSITLLGVIGNSLVIRHVIFKFSMRTVTNFFIANLAVADLLVNTLCPLPTL 108  
 Query 102 VNDLITGMFPFNATCKMSGLVQGMVSASVFTLVAIAVERFCIVHFFPREKLIRKALVT 161  
 L+ M C + QG+V S TL IR+R RCIV K+ R + +  
 Sbjct 109 TTYLGMGKMGVFLCHLVPAQGLAVGVSTITLTVIALDRHRCIVYHLESKISKRISFLI 166  
 Query 162 IAVIALALLIMCPSAVTLTVTREHHFMDARNRSPYLYSCWAMP--EKGR-RVYT 218  
 I + M ++L+ P L + RE ++ + + C E WP EK + VY+  
 Sbjct 169 IGLWRISALLASP---LAIFREYSLIEIIP---DFEIVACTEWPGEERKISYGVYSEL 221  
 Query 219 VLFSHIYALPLALIVVMYARIARLCOAPGAGEAADPRASRRRARVVMHVAWVAF 278  
 Y+ PL +I Y RI KL P A+ ++RR + MLV Y +  
 Sbjct 222 SLLILTVPLIGIISFSYTRINSLKSHVSPG-----AANDHYQRORQRTIMLCVGVVV 276  
 Query 279 FTLSNLPALWALLLLIDYQG--LSAPQLHLTVYAPFAHNLAFPNSSANPIIYGVFNENF 336  
 F +SNLPL A L +D L + L+ P H A ++ANP++YG+ N N+  
 Sbjct 277 FAVSWPLHAFQLAVIDDSQVLDLKEYLKI---FTVFHIIAMCTIFANFLYGVNNSNY 332  
 Query 337 RRGFOAARFARLCRPSGSKE 358  
 R+ F +FR R H R  
 Sbjct 333 RKAFLSAFRCE--QRDLAIRSE 352

>gb|AAA5920.1| **C** neuropeptide y receptor  
 Length=384  
 GENE ID: 4886 NPY1R | neuropeptide Y receptor Y1 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 160 bits (405), Expect = 8e-39, Method: Compositional matrix adjust.  
 Identities = 106/316 (33%), Positives = 162/316 (51%), Gaps = 17/316 (5%)  
 Query 41 EVAAMFIVA--YALIFLLCMVGNLTLCVFLVKNRHMRTVTNMFILNLAVSLDLGIFCM 98  
 P+P +P +A Y + +L + GN + I+LK + M VTN+ I+NL+ SDDL I C+P  
 Sbjct 36 PLAMIFTLALAYGAVILLGVSGNLALIIILKQKMRNVNITLIVLSFDDLVAIMCLP 95  
 Query 99 TLDVNLITGMFPFNATCKMSGLVQGMVSASVFTLVAIAVERFCIVHFFPREKLIRKALVT 158  
 T V L+ M F A CK+ VQ +S+ S+FLV IAVR+ I+P + R A  
 Sbjct 96 LTFVYTMDDHNVFGEAMCKMNFVQCVSITVSIFSLVIAVERHQLINFGNRPNHRHA 155  
 Query 159 LVTVIAVIALALLIMCPSAVTLTVTRE--HHFMDARNRSPYLYSCWAMPGEKGRVYT 217  
 V IAVI L+ P + +T E + +DA Y C++ +P R Y T  
 Sbjct 156 YVGIVAVHVLAVASSLFLTVQVNTDEPFQNVTLDAKDKYV---CFDPFSDSHRLSYT 212  
 Query 218 VTLFSHIYALPLALIVVMYARIARLCOAPGAPGAGEAADPRASRRRARVVMHVAWVAF 277  
 TL L Y PL I + Y I +L + + + + +R + ML+ +  
 Sbjct 213 TLLILVAYPDCICPICTYPIYVIRLDRNMDGEMKMYKRSSTRKRI--MLLSITV 270  
 Query 278 FTLNLPALWALLLLIDYQG--LSAPQLHLTVYAPFAHNLAFPNSSANPIIYGVFNENF 336  
 F +SNLPL A L +D L + L+ P H A ++ANP++YG+ N N+  
 Sbjct 271 AFVSWPLTLPTNTYFDNKHQIATCNHNL---LFLCHLTAMISTCVNPIFYGLNKNF 327  
 Query 337 RRGFO-----AAFR 347  
 +R Q FR+R  
 Sbjct 328 QRDLQFFMFCRFR 343

>ref|NP\_000900.1| **U** **C** neuropeptide Y receptor Y1 [Homo sapiens]  
 sp|P25929.1|NPY1R HUMAN **C** RecName: Full=Neuropeptide Y receptor type 1; AltName: Full=NPY-1R  
 gb|AAA73215.1| **C** (Human neuropeptide Y peptide YY receptor mRNA, complete cds.),  
 gene product

8 more sequence titles

gb|AAAS9447.1| **[G]** neuro peptide Y receptor Y1  
 gb|AAAS6657.1| **[G]** Neuro peptide Y receptor Y1 [Homo sapiens]  
 gb|AAAS5647.1| **[G]** neuro peptide Y1 receptor [Homo sapiens]  
 gb|AAH1720.1| **[G]** Neuro peptide Y receptor Y1 [Homo sapiens]  
 gb|BAK04841.1| **[G]** neuro peptide Y receptor Y1 [Homo sapiens]  
 dbj|BAJ35472.1| **[G]** unnamed protein product [Homo sapiens]  
 Length=384

GENE ID: 4886 NPY1R | neuro peptide Y receptor Y1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 160 bits (404), Expect = 1e-38, Method: Compositional matrix adjust.  
 Identities = 106/316 (33%), Positives = 162/316 (51%), Gaps = 17/316 (5%)

Query 41 PVAMFPIVA--YALIFLLCMVMTLVCFIVLKNRHHMTVNNPILNLAVSDLLVIGPCMP 98  
 P+A P+ A+ Y + +L+ GN + I+LX+ M VTN+ I+NL+ SDLV+ I C+P  
 Sbct 36 PLAMIFTLALAYGAVILVSGNMLALIIILKOKEMHNTNINLVNLSFSDLVAIMCLP 95  
 Query 99 TILVDNLTITWPFNDATCKMSGLVQGMVSASVPTLVAIAVERFCIVHPPEKILTRKA 158  
 T V L+ W F A CR++ VQ+S++ S+P+LV IAVR+ I++P + R A  
 Sbct 96 PFTVTLAVHVPGRMCLMPPVQCVSTIVSIFSLVIAVERGSLIINPGRWRPNRDA 155  
 Query 159 LVTIAMALLALIMCPASVTLTVTRE--NHPMVDAERNRYPLTSCWEAWPEKMRVYT 217  
 V IAVI+ LA+ P + +T E + +DA Y C++ +P R YT  
 Sbct 156 YGVIAIVLWIAVASSLPFLIVQMTDEFQNVTLQAYKKYV---CPDPPSDSHRLSYT 212  
 Query 218 TVLFSHIYLAFLAVIMVYARIARKLCOAPGPAPGGEAAADPRASRRRVRVHMLVVAL 277  
 T+L Y PL I+ Y +I +D+ + + + +R + +M++ +  
 Sbct 213 TLLVLVYFGPLCFIPICYPKIVYILKRRKRNMDKMDKRYSSSETRKINI--MLLSIV 270  
 Query 278 PFTLSMLPLWALLLLIDYQ--LSAPQLMLTVYAPFARHAFNNSANPIIYGYNENF 336  
 F + WFL+ P A+ + GN LVC + +K+ MH+ T+P+I+NLAV+D+++ + P TL  
 Sbct 271 AFACWMLPLTIPMTVFDNHNLIATCNHNL---LPLLCHLTAMISTCVNPIFYGFLNKNF 327  
 Query 337 RRGPO-----AAFRAR 347  
 +R Q FR+R  
 Sbct 328 QRDLLFFNFPCDFRSR 343

-gb|AAB43705.1|AF236081.1 **[G]** orphan G-protein coupled receptor GPR72 [Homo sapiens]  
 Length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/322 (32%), Positives = 166/322 (51%), Gaps = 22/322 (6%)

Query 42 VAAMFIVAYALIFLPCVGNITVCFIVLKNRHHMTVNNPILNLAVSDLLVIGPCMPPTL 101  
 V A+ IYAV+ I + + GN LVC + +K+ MH+ T+P+I+NLAV+D+++ + P TL  
 Sbct 70 VKALLIYVAFSIIIVFSLPGNVLVCHVIFKQRMHSATSLFIVNLVADIMITLNTLPTL 129  
 Query 102 VDNLTITWPFNDATCKMSGLVQGMVSASVPTLVAIAVERFCIVHPPEKILTRKALVT 161  
 V + + W F C +S O S+ S TL AIAV+R + I+HP + +++ K ++  
 Sbct 130 VRVNSTWIPGKGMCHVSRFAOYCSLHVSALTLTIAVDHROVIMHPLKPRISTKGVY 189  
 Query 162 IAVINALALLIMCPASVTLTVTREHHFMDARNRSYPLTSCWEAWPEK--MRVYTVT 219  
 IAVI+ VA+ P A+ + GN LVC + +K+ MH+ T+P+I+NLAV+D+++ + P TL  
 Sbct 190 IAVINMTATFSLHAIQCKLFTFKYS---EDIVRSL---CLDPFPEPADLFWKYLDLA 242  
 Query 220 LFSHIYLAFLAVIMVYARIARK--LCOAPGPAPGGEAAADPRASRRRVRVHMLVVAL 277  
 P +Y+ PL +I V YAR+A+K LC G + A R++ + +ML++V +  
 Sbct 243 FTILLIYILPLIIIVAYARAKKMLWLNHMDGVTEQYFA---LRRKKKTIKMLLVVV 299  
 Query 278 PFTLSMLPLWALLLLIDYQ--LSAPQLMLTVYAPFARHAFNNSANPIIYGYNENF 337  
 F L W PL +LL LS+ + F F HW A + + NP IV + NHRF  
 Sbct 300 LEALCHPLNCFVLL---LSKVIKTNNALVYAF--HFMASSTCTNPFIVLQKNGFR 353  
 Query 338 RRGQAAFRARLCPPSGSHKKA 359  
 +A +C RP ++  
 Sbct 354 IELKALL--SMCRPPKQEDG 373

-sp|Q9NTM4.2|GPR83\_HUMAN **[G]** RecName: Full=Probable G-protein coupled receptor 83; AltName:  
 Full=G-protein coupled receptor 72; Flags: Precursor

gb|AAH67473.1| **[G]** G protein-coupled receptor 83 [Homo sapiens]  
 gb|BAW6929.1| **[G]** G protein-coupled receptor 83 [Homo sapiens]  
 dbj|BAJ37605.1| **[G]** unnamed protein product [Homo sapiens]  
 Length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAMFIVAYALIFLPCVGNITVCFIVLKNRHHMTVNNPILNLAVSDLLVIGPCMPPTL 101  
 V A+ IYAV+ I + + GN LVC + +K+ MH+ T+P+I+NLAV+D+++ + P TL  
 Sbct 70 VKALLIYVAFSIIIVFSLPGNVLVCHVIFKQRMHSATSLFIVNLVADIMITLNTLPTL 129  
 Query 102 VDNLTITWPFNDATCKMSGLVQGMVSASVPTLVAIAVERFCIVHPPEKILTRKALVT 161  
 V + + W F C +S O S+ S TL AIAV+R + I+HP + +++ K ++  
 Sbct 130 VRVNSTWIPGKGMCHVSRFAOYCSLHVSALTLTIAVDHROVIMHPLKPRISTKGVY 189  
 Query 162 IAVINALALLIMCPASVTLTVTREHHFMDARNRSYPLTSCWEAWPEK--MRVYTVT 219  
 IAVI+ VA+ P A+ + GN LVC + +K+ MH+ T+P+I+NLAV+D+++ + P TL  
 Sbct 190 IAVINMTATFSLHAIQCKLFTFKYS---EDIVRSL---CLDPFPEPADLFWKYLDLA 242  
 Query 220 LFSHIYLAFLAVIMVYARIARK--LCOAPGPAPGGEAAADPRASRRRVRVHMLVVAL 277  
 P +Y+ PL +I V YAR+A+K LC G + A R++ + +ML++V +

Sbjct 243 TFFLLVILPLLIIISVAYARVAKKMLCNMIGDVTTEQYFA---LRKKKKTIKMLMLVVV 299  
 Query 278 FFTLSWLPALLLLIDYQGLSAPQLHLVTVYAPFAHMLAFNNSAMPIIYGYFNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IY + NENFR  
 Sbjct 300 LFLCWFPLNLCYVLL-----LSSKVRTNNALYFAP-HWFAMSTCYNPFYICWLNENFR 353  
 Query 338 RGQQAARFRLCPRPGSGSHE 358  
 +A +C RP ++  
 Sbjct 354 IELKALL--SMCQRPKPKQED 372

>ref|NP\_057624.2| **G** G protein-coupled receptor 83 [Homo sapiens]

gb|ABY87919.1| **G** G protein-coupled receptor 83 [Homo sapiens]

length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAMFIVAYALIFLLCMVGNLTVCVILKNRHMHTVTNMFILNLAVSDLVIGFCMPFTTL 101  
 V A+ IYAV+ I + + GN LVC + K+ H+ T+P+NLAVD+ + + P TL  
 Sbjct 70 VKALLIVAYSFIIVPSLFGVNLVCHVIFKQRMHSA TSLFIVNLAVADIMTILMTPTTL 129  
 Query 102 VDNLTGHPDNATCKMSGLVQMSVSASVPTLVAIAVERFCIVHPREKILTRKALVT 161  
 V + N F C +S Q S+ TL AIAR+ I+HP +++++ K ++  
 Sbjct 130 VRFVNSTWIFGKGMCHVSFRQAQYCSLHVSALTLTAIADVRHQVMHPLKPRISITGVYI 219  
 Query 162 IAVIMALLIMCPSAVTLTVTREHHFMVDARNRSYPLYSCEWAMPEKG--MRRVYTV 189  
 IAVIN +A P A+ + + + RS C +PE  
 Sbjct 190 IAVIMATMFFSLPHAIQCKLFTFKYS--EDIVRSL---CLPDFPEADLFWKYLDLA 242  
 Query 220 LFSHYLAPLALIVMYARIAR--LQAPGAPGQGEAADPRASRRARVVMILVMVAL 277  
 P +Y+ PL +I V YAR+A K LC G + A R++ + ML++V +  
 Sbjct 243 TFIILYILPLLIIISVAYARVAKKMLCNMIGDVTTEQYFA---LRKKKKTIKMLMLVVV 299  
 Query 278 FFTLSWLPALLLLIDYQGLSAPQLHLVTVYAPFAHMLAFNNSAMPIIYGYFNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IY + NENFR  
 Sbjct 300 LFLCWFPLNLCYVLL-----LSSKVRTNNALYFAP-HWFAMSTCYNPFYICWLNENFR 353  
 Query 338 RGQQAARFRLCPRPGSGSHE 358  
 +A +C RP ++  
 Sbjct 354 IELKALL--SMCQRPKPKQED 372

>dbj|BAA96064.1| **G** KIAA1540 protein [Homo sapiens]

length=424

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAMFIVAYALIFLLCMVGNLTVCVILKNRHMHTVTNMFILNLAVSDLVIGFCMPFTTL 101  
 V A+ IYAV+ I + + GN LVC + K+ H+ T+P+NLAVD+ + + P TL  
 Sbjct 71 VKALLIVAYSFIIVPSLFGVNLVCHVIFKQRMHSA TSLFIVNLAVADIMTILMTPTTL 130  
 Query 102 VDNLTGHPDNATCKMSGLVQMSVSASVPTLVAIAVERFCIVHPREKILTRKALVT 161  
 V + N F C +S Q S+ TL AIAR+ I+HP +++++ K ++  
 Sbjct 131 VRFVNSTWIFGKGMCHVSFRQAQYCSLHVSALTLTAIADVRHQVMHPLKPRISITGVYI 219  
 Query 162 IAVIMALLIMCPSAVTLTVTREHHFMVDARNRSYPLYSCEWAMPEKG--MRRVYTV 189  
 IAVIN +A P A+ + + + RS C +PE  
 Sbjct 191 IAVIMATMFFSLPHAIQCKLFTFKYS--EDIVRSL---CLPDFPEADLFWKYLDLA 243  
 Query 220 LFSHYLAPLALIVMYARIAR--LQAPGAPGQGEAADPRASRRARVVMILVMVAL 277  
 P +Y+ PL +I V YAR+A K LC G + A R++ + ML++V +  
 Sbjct 244 TFIILYILPLLIIISVAYARVAKKMLCNMIGDVTTEQYFA---LRKKKKTIKMLMLVVV 300  
 Query 278 FFTLSWLPALLLLIDYQGLSAPQLHLVTVYAPFAHMLAFNNSAMPIIYGYFNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IY + NENFR  
 Sbjct 301 LFLCWFPLNLCYVLL-----LSSKVRTNNALYFAP-HWFAMSTCYNPFYICWLNENFR 354  
 Query 338 RGQQAARFRLCPRPGSGSHE 358  
 +A +C RP ++  
 Sbjct 355 IELKALL--SMCQRPKPKQED 373

>gb|AAH87474.1| **G** G protein-coupled receptor 83 [Homo sapiens]

length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]

(10 or fewer PubMed links)

Score = 152 bits (385), Expect = 2e-36, Method: Compositional matrix adjust.  
 Identities = 103/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAMFIVAYALIFLLCMVGNLTVCVILKNRHMHTVTNMFILNLAVSDLVIGFCMPFTTL 101  
 V A+ IYAV+ I + + GN LVC + K+ H+ T+P+NLAVD+ + + P TL  
 Sbjct 70 VKALLIVAYSFIIVPSLFGVNLVCHVIFKQRMHSA TSLFIVNLAVADIMTILMTPTTL 129  
 Query 102 VDNLTGHPDNATCKMSGLVQMSVSASVPTLVAIAVERFCIVHPREKILTRKALVT 161  
 V + N F C +S Q S+ TL AIAR+ I+HP +++++ K ++  
 Sbjct 130 VRFVNSTWIFGKGMCHVSFRQAQYCSLHVSALTLTAIADVRHQVMHPLKPRISITGVYI 189  
 Query 162 IAVIMALLIMCPSAVTLTVTREHHFMVDARNRSYPLYSCEWAMPEKG--MRRVYTV 219  
 IAVIN +A P A+ + + + RS C +PE  
 Sbjct 190 IAVIMATMFFSLPHAIQCKLFTFKYS--EDIVRSL---CLPDFPEADLFWKYLDLA 242  
 Query 220 LFSHYLAPLALIVMYARIAR--LQAPGAPGQGEAADPRASRRARVVMILVMVAL 277  
 P +Y+ PL +I V YAR+A K LC G + A R++ + ML++V +  
 Sbjct 243 TFIILYILPLLIIISVAYARVAKKMLCNMIGDVTTEQYFA---LRKKKKTIKMLMLVVV 299  
 Query 278 FFTLSWLPALLLLIDYQGLSAPQLHLVTVYAPFAHMLAFNNSAMPIIYGYFNENFR 337  
 P L W PL +LL LS+ + F F HW A ++ NP IY + NENFR

Sbjct 300 LFLCWFPLNLYVLL----LSKVRTNIALYFAP-HWFMSTCTNPIYCHLVNENFR 353  
 Query 338 RGFQALFRARLCRRPSPGSHK 358  
 +A +C R P  
 Sbjct 354 IELKALL--SMCQRPPKQED 372

>gb|AAI28134.1| **[G]** GPR103 protein [Homo sapiens]  
 Length=356

GENE ID: 84109 QRPRF | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 149 bits (375), Expect = 2e-35, Method: Compositional matrix adjust.  
 Identities = 84/281 (29%), Positives = 144/281 (51%), Gaps = 21/281 (7%)

Query 74 MHTVNTMFIINLAVSDLVGIFCMPTTLVDNLITOMFPDNATCKMSGLVQMSVASVFT 133  
 M TVTN+FI +L+SDLL+ PC+P T++ N+ W CKM VQ +V +T  
 Sbjct 1 MHTVNTMFIINLAVSDLLITFFCIPTVTLQNTSDNLWGGAFICMVPFVQSTAVVTEILT 60  
 Query 134 LVAIAVERPRCIVHPFREK--LTLRKALVTIAVIALALLIMCP--SAVTLVTREEHF 189  
 +AVER +VHPF K T R+ + VAV +R++ P L + + F  
 Sbjct 61 MTCIAVERHQGLVHPFMKQYTNRRAPITMLGVNMLVAVIVGSPMHHVOGLEI--KYDF 117  
 Query 190 MVDARNRSPFLYSCNEMPEKMRVYITLFSHYLAPALIVMYARIKLCQAQFP 249  
 + + + C B W +++YT + +L PL +++++Y+I +L  
 Sbjct 118 LYEKEH----ICCLSEMTSPVHQKIYITFILVILLPLM/VNLIYSKIGYELMIKKRV 172  
 Query 250 APG-----GREADPRASRRARVVMVLVVFLLTSLVPLWALLLLIDYQGLSAPQ 302  
 G +L+ + +R+ R V M+V V F + M P + +L Y  
 Sbjct 173 GDSGLVLTTHQKES--KLRKCKRANIMVTVVAFVACVWHPFVIMHIESNPEKEY 230  
 Query 303 LHLVTYVYFAPFAMHAPNSANPIIYGYPHNFRGQAA 343  
 P + F NS NPI+Y + NENF+ + A  
 Sbjct 231 DQVTKIMFATVOIGFSPSNCINPIVYAPNENFKCNVSSA 271

>ref|NP\_003848.1| **[U]** **[G]** galanin receptor 2 [Homo sapiens]

sp|Q43603.1|GALR2\_HUMAN **[G]** RecName: Full=Galanin receptor type 2; AltName: Full=GALR2;  
 AltName: Full=GALR2

gb|AAC39634.1| **[G]** galanin receptor GalR2 [Homo sapiens]  
 10 more sequence titles

gb|AAC18118.1| **[G]** galanin receptor subtype 2 [Homo sapiens]  
 gb|AAC35587.1| **[G]** galanin receptor type 2 [Homo sapiens]  
 gb|AAD08671.1| **[G]** galanin receptor type 2 [Homo sapiens]  
 gb|AAH69130.1| **[G]** Galanin receptor 2 [Homo sapiens]  
 gb|AAH74914.1| **[G]** Galanin receptor 2 [Homo sapiens]  
 gb|AAH74915.1| **[G]** Galanin receptor 2 [Homo sapiens]  
 gb|AAI09053.1| **[G]** Galanin receptor 2 [Homo sapiens]  
 gb|AAI09052.1| **[G]** Galanin receptor 2 [Homo sapiens]  
 gb|EAW89364.1| **[G]** galanin receptor 2 [Homo sapiens]  
 gb|ABQ52421.1| **[G]** galanin receptor 2 [Homo sapiens]  
 Length=387

GENE ID: 8811 GALR2 | galanin receptor 2 [Homo sapiens] (Over 10 PubMed links)

Score = 148 bits (374), Expect = 3e-35, Method: Compositional matrix adjust.  
 Identities = 122/373 (32%), Positives = 181/373 (48%), Gaps = 42/373 (11%)

Query 41 PVAMFIVAYALIFLLCMVGNITLVCPILKNRHHMTVNTMFIINLAVSDLVGIFCMPTT 100  
 P A + + +ALIFL+ VGNITLV +L+ + TN+PIAL VIDL + C+P  
 Sbjct 23 PEAVIVFLPALIFLVGTVGNITLVAVLLGGQAVSTTMLPIINLAVADLCIFLCVFPQ 82  
 Query 101 LVNMLITOMFPDNATCKMSGLVQMSVASVFTLVAIAVERPRCIVHPF--REKILTKRA 158  
 + GN P + CK + +AS TPL A++R+ I +P RS T R A  
 Sbjct 83 ATIYTLGDFVGSILCKAVHPLFLTMHASSFTLAAVSLORYLAIRYPLHSRELATPRNA 142  
 Query 159 LVTIAVINALALLIMCPASVTLTVTREHHFMDARNRSPFLYSCNEMPEKMRVYIT 218  
 L I +IM L+LL P L+ R+ ++ L C AN RR  
 Sbjct 143 LAAITGLINGLSILFSGP---YLSYRQ-----SQLANLTVCHPAMSAP--RRRAMDI 169  
 Query 219 VLSHYLAPALIVMYARIKLCQAQPGAPGEEAADPRASRRARVVMVLVVFLL 278  
 F VL P+ + CK + R L + A P AD A R + +V H++V+  
 Sbjct 190 CTFVSYLLPVVLGLTYARTLRYLKRADVP----AAGSGARRAKRVTMRMLIVAA 244  
 Query 279 FTLMLPLMALLLLIDYQGLSAPQLHLVTYVYF--FAHMLAFNSSANPIIYGYPHNFR 337  
 F L M+P AL+L + +GO + YA +H ++ NS NPI+Y ++PR  
 Sbjct 245 FCLCMHMHAILILCVFQPLTR----ATYALRILSHLVSYANSCVNPVIALVSKHFR 300  
 Query 338 RGF-----QAQFRA--RLCPSPGSHKEAYSERPG--LLH--RVFVVRVPSDGLP 384  
 +GF +A RA R+R+ G+H + ER LLH +RP P  
 Sbjct 301 KQFTICAGLIGRAFAPRASGRVCAAARQTSQSVLEESDILLHSGAAGALPC---P 356  
 Query 365 SESQPSGAPFPQ 397  
 S P P PG  
 Sbjct 357 GASQPCILEPCPQ 369

>gb|AAB05897.1| **[G]** neurokinin-2 receptor  
 Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 148 bits (373), Expect = 4e-35, Method: Compositional matrix adjust.  
 Identities = 117/408 (28%), Positives = 185/408 (45%), Gaps = 25/408 (6%)

Query 21 NTEATPATLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNITLVCPILKNRHHMTVTNM 80  
 N + P +N T ++ + S A++ AY + L+ + GN +V +L+ R M TVTN





Query 292 LIDYQQLSAPQLHLVTVAFFPAHWAFFNSSANPIIYGVFNNRFRGFQAAF 344  
 Y SA + + F L + + S NPIIY + N+ FR GF A F  
 Sbjct 335 WRAYDTASAEK--RLSGTPIPIILLLYTSSCVNPIIYCFNKRRLFLGPMATF 395

>sp|P21452.2|NK2R\_HUMAN [G] RecName: Full=Substance-K receptor; Short=SKR; AltName: Full=Neurokinin A receptor; AltName: Full=NK-2 receptor; Short=NK-2R;  
 gb|AA280303.1| neurokinin-2 receptor, NK-2 receptor [human, Peptide, 398 aa]  
 gb|BAF84358.1| tachykinin receptor 2 [Homo sapiens]  
 gb|BAW54324.1| tachykinin receptor 2, isoform CRA\_a [Homo sapiens]  
 dbj|BAF84685.1| unnamed protein product [Homo sapiens]  
 Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 146 bits (369), Expect = 1e-34, Method: Compositional matrix adjust.  
 Identities = 117/408 (28%), Positives = 184/408 (45%), Gaps = 25/408 (6%)

Query 21 NTEATPATNLTFSSYQHTSPVAMFIVAYALIFLLQVGNITLVCPIVLNRRHRTVTNM 80  
 N + + S N NPIIY + S A + + AY + L + GR V + I + L + R M TTN  
 Sbjct 11 NISSGPESNTTGITAFSPMSQALWAPAYALVAVTGNATVIMILAHRRMRTVTNY 70

Query 81 FIHLAVSDDLGVIFCMPTTLVDNLITGMPDNATCKMSGLVQMSVSASVFTLVAIAVE 140  
 FI+NLA++DL + P V W F A C L + + S + + + AIA +  
 Sbjct 71 FIVNLALADLCAAFAFNAPFVYASHNIWYGRACFYQNLFPITAMFVSIYSTAIAAD 130

Query 141 RFRICVHPFREKLTLRKALVTIAVWALLIMCPSAVTLTTRERHHFVMDARNRSYPL 200  
 R + IYRFP + L + A IN +AL + + P T V + +  
 Sbjct 131 RYMAIYHPFOPRLSASTKAVIAGIWLALALASPCQCYSTVTMDQ-----GA 178

Query 201 YSCWEANPEKGMHR--VYTTVLFPSHIYLAFLAVIMVYARIARKLCAQAPAPGGEA- 256  
 C AMPE + + Y V + + IY PL + + V + I L + P G + A  
 Sbjct 179 TKCVANRDSGGKTLILYHIVVIALIYFLPAMVFAVSIGTLWRRAVP--GHQAH 235

Query 257 -ADPRASRRARVHMLVAFLLFTLSLPLWALLLLIDYQQLSAPQLHLVTVAFFPAH 315  
 A+ R + + + V +V+L F + MLF +L + + + VV F  
 Sbjct 236 GSNRLQELQCKVKTWVVLVLTFAICLFPVHLFIIGSPQDIYCHKFIQOYTLALF-- 293

Query 316 WLAFFNSSANPIIYGVFNNRFRGFQAFARLRCFPGSGHKEAYSERPGOLLHRRVTVV 375  
 WLA + + NPIIY N FR GF AFR CP + + + + P L RV  
 Sbjct 294 WLAMSTNYNPIIYCNLHRRFRSGFLAFC--CPWVTPTKDKLELTPTTSLTRVNR 351

Query 376 VRPSDGLSPESGPSGAPRPGRLPLNGRVAHHGLFRPGCGCSHLPL 423  
 + + PS P + + G G P +H+ +  
 Sbjct 352 HTKETLPMAGDTASATSSEAGRP-QDQSGLWFGYLLATPTKTHVEI 398

>gb|AAC31760.1| [G] neurokinin A receptor [Homo sapiens]  
 gb|AAA60347.1| neurokinin A receptor  
 Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
 Identities = 117/408 (28%), Positives = 184/408 (45%), Gaps = 25/408 (6%)

Query 21 NTEATPATNLTFSSYQHTSPVAMFIVAYALIFLLQVGNITLVCPIVLNRRHRTVTNM 80  
 N + + S N NPIIY + S A + + AY + L + GR V + I + L + R M TTN  
 Sbjct 11 NISSGPESNTTGITAFSPMSQALWAPAYALVAVTGNATVIMILAHRRMRTVTNY 70

Query 81 FIHLAVSDDLGVIFCMPTTLVDNLITGMPDNATCKMSGLVQMSVSASVFTLVAIAVE 140  
 FI+NLA++DL + P V W F A C L + + S + + + AIA +  
 Sbjct 71 FIVNLALADLCAAFAFNAPFVYASHNIWYGRACFYQNLFPITAMFVSIYSTAIAAD 130

Query 141 RFRICVHPFREKLTLRKALVTIAVWALLIMCPSAVTLTTRERHHFVMDARNRSYPL 200  
 R + IYRFP + L + A IN +AL + + P T V + +  
 Sbjct 131 RYMAIYHPFOPRLSASTKAVIAGIWLALALASPCQCYSTVTMDQ-----GA 178

Query 201 YSCWEANPEKGMHR--VYTTVLFPSHIYLAFLAVIMVYARIARKLCAQAPAPGGEA- 256  
 C AMPE + + Y V + + IY PL + + V + I L + P G + A  
 Sbjct 179 TKCVANRDSGGKTLILYHIVVIALIYFLPAMVFAVSIGTLWRRAVP--GHQAH 235

Query 257 -ADPRASRRARVHMLVAFLLFTLSLPLWALLLLIDYQQLSAPQLHLVTVAFFPAH 315  
 A+ R + + + V +V+L F + MLF +L + + + VV F  
 Sbjct 236 GSNRLQELQCKVKTWVVLVLTFAICLFPVHLFIIGSPQDIYCHKFIQOYTLALF-- 293

Query 316 WLAFFNSSANPIIYGVFNNRFRGFQAFARLRCFPGSGHKEAYSERPGOLLHRRVTVV 375  
 WLA + + NPIIY N FR GF AFR CP + + + + P L RV  
 Sbjct 294 WLAMSTNYNPIIYCNLHRRFRSGFLAFC--CPWVTPTKDKLELTPTTSLTRVNR 351

Query 376 VRPSDGLSPESGPSGAPRPGRLPLNGRVAHHGLFRPGCGCSHLPL 423  
 + + PS P + + G G P +H+ +  
 Sbjct 352 HTKETLPMAGDTASATSSEAGRP-QDQSGLWFGYLLATPTKTHVEI 398

>ref|NP\_005963.3| [L]G pancreatic polypeptide receptor 1 [Homo sapiens]  
 sp|P50391.1|NPY4R\_HUMAN [G] RecName: Full=Neuropeptide Y receptor type 4; Short=NPY4-R; AltName: Full=Pancreatic polypeptide receptor 1; Short=PP1  
 gb|AAC50280.1| neuropeptide Y4 receptor protein  
 emb|CAA51433.1| pancreatic polypeptide receptor PPI [Homo sapiens]  
 gb|AAF23199.1| pancreatic polypeptide receptor 1 [Homo sapiens]  
 emb|CAI13318.1| pancreatic polypeptide receptor 1 [Homo sapiens]  
 gb|AAV68197.1| pancreatic polypeptide receptor 1 [Homo sapiens]  
 Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
 Identities = 103/336 (30%), Positives = 167/336 (49%), Gaps = 19/336 (5%)

Query 14 PLSQNGTNTATPATNLTFSSYQHTSPVAMPIVAYALIFLVCWGHTLVCFVILQKRNH 73  
 P S G N T T P S + Q + V + +Y++ ++ +GN + + + +  
 Sbjct 12 PKSPQGNRSKPLPTPNFSEHQDSVDVMVFVITSYSETVVGVLGNLCLMCVTRQKE 71

Query 74 MHTVNMPIFLNALVSDLLVGFPCMPITLWNLITGWPFNDATCKMSGLVQMSVSASVPT 133  
 VTN+ I NLA SD L+ + C P T V + + W F CMS +Q MSV+ S+ +  
 Sbjct 72 KANVTNLINLARIASDFLMCLLQPLTAVTINDVYIFGEBLCKMSAFIQCHSVTVSILS 131

Query 134 LVAIAVERFCIVHPFREKLTKALVTIAVINALALLIMCP---SAVTLVTRREEH--- 187  
 LV +A+ER +I+P K++ +A + I +W +A++ P +++ V + H  
 Sbjct 132 LVVLVALERHQILNTPGWKPSISQAYLGIVLIVIACTVLSPLFLANSILENVPHKNSKA 191

Query 188 -HFVMDARNRSYPLSCWEAMPEKGMRRVYITVLFHSIYALPLALIVMYARIARLKQA 246  
 F+ D C E+WP R +YTT L Y PL I+V YARI R+L+  
 Sbjct 192 LEFLADK-----VVCESWPLAHRTITVTLFLLPQYCLPLGFIIVCTARIYRLQRO 244

Query 247 PGPAQGEAADPRASRRARVRVHMLVVALPFTLSWPLMALALLIDYQQLSAPQLHLV 306  
 G + RA + +V +LV++ + F + WLPL L D+ + P H  
 Sbjct 245 GRVPHKGYSL--RAGHK-QVNVLVVMVAVFVLMPLHIVFNSLEDWHEATIPICHGN 301

Query 307 TVYAPFAHMLAFNSSANPIIYGFNENPERGQA 342  
 + F H LA ++ NP IYG+ N NP++ +A  
 Sbjct 302 LI--FLVCHLLAASCTCVNFIYGLNPLNPKKEKA 335

>ref|NP\_001048.2| **[G]** tachykinin receptor 2 (Homo sapiens)  
 dbj|BAC05952.1| **[G]** seven transmembrane helix receptor (Homo sapiens)  
 Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 (Homo sapiens)  
 (Over 10 PubMed links)

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
 Identities = 117/408 (28%), Positives = 183/408 (44%), Gaps = 25/408 (6%)

Query 21 NTEATPATNLTFSSYQHTSPVAMPIVAYALIFLVCWGHTLVCFVILQKRNHMTVM 80  
 N + P + N T + + S A++ AY + L+ + GN +V +I+L+R M TVTN  
 Sbjct 11 NISSGQESNTTGTAPSPMSQIALMATAYALVAVTGNIAVINILAHRRMRTVNY 70

Query 81 FILNALVSDLLVGFPCMPITLWNLITGWPFNDATCKMSGLVQMSVSASVTLVAIVE 140  
 F+ NLA+DL + F V + W F A C L ++ S+++ AIA+  
 Sbjct 71 FIVNLALDLQALPNAAPNFVYASHNIWYGRACVYQNLPIITAMPVETIYSHLAAJ 130

Query 141 RFRICVHPFREKLTKALVTIAVINALALLIMCPSAVTLVTRREEHFNVDARNRSYPL 200  
 R+ IURP +V +Y+V L F + WLP +L + + + YV F  
 Sbjct 131 RYMAIVHPPOPLASPTKAVIAGIWLVALALASQCFYSTVINDQ-----GA 178

Query 201 YSCWEAMPEKGMRR---VITVLFHSIYALPLALIVMYARIARLKQAQPGAPGGERA 256  
 C AWPE + +Y V+ + IY PLA++ V + I L+ + P G +A  
 Sbjct 179 TKCVVAMPEDSGOKTLLLYHLVIALIYPLVPLVMPVAVSYGLTMRRAVP---GHQAH 235

Query 257 -ADPRASRRARVRVHMLVVALPFTLSWPLMALALLIDYQQLSAPQLHLVTVYAPFAH 315  
 A+ IURP +V +Y+V L F + WLP +L + + + YV F  
 Sbjct 236 GANLRHLQAMKFPKTVNLVLTFAICLPYHLVYLGSPQDIYCHKEFIQOQVYLALF-- 293

Query 316 WLAFNNSANPIIYGFNENPERGQAQFARLCPSPSGHKEAYSPGGLHREVPV 375  
 WLA ++ NP IYI N FR GP+ APR CP + + + P I RV  
 Sbjct 294 WLANSSTMYNPIIYCLNHRFSRGLAFRC--CPWVTPKDEKLEITPTLSLRVNRKC 351

Query 376 VRPDSGLPSESQSGAPRGLPLNGRVAHGLPREGGCSHLPL 423  
 + + + FS P +G G P +R+ +  
 Sbjct 352 HKTETLPMAGTASATSEASGRP-QQSGLMFVGLAPLAPTKVEI 398

>gb|AA07759.1| **[G]** pancreatic polypeptide receptor  
 gb|AAV68196.1| **[G]** pancreatic polypeptide receptor 1 (Homo sapiens)  
 gb|AAH6238.1| **[G]** Pancreatic polypeptide receptor 1 (Homo sapiens)  
 Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 (Homo sapiens)  
 (Over 10 PubMed links)

Score = 145 bits (365), Expect = 3e-34, Method: Compositional matrix adjust.  
 Identities = 103/336 (30%), Positives = 167/336 (49%), Gaps = 19/336 (5%)

Query 14 PLSQNGTNTATPATNLTFSSYQHTSPVAMPIVAYALIFLVCWGHTLVCFVILQKRNH 73  
 P S G N T T P S + Q + V + +Y++ ++ +GN + + + +  
 Sbjct 12 PKSPQGNRSKPLPTPNFSEHQDSVDVMVFVITSYSETVVGVLGNLCLMCVTRQKE 71

Query 74 MHTVNMPIFLNALVSDLLVGFPCMPITLWNLITGWPFNDATCKMSGLVQMSVSASVPT 133  
 VTN+ I NLA SD L+ + C P T V + + W F CMS +Q MSV+ S+ +  
 Sbjct 72 KANVTNLINLARIASDFLMCLLQPLTAVTINDVYIFGEBLCKMSAFIQCHSVTVSILS 131

Query 134 LVAIAVERFCIVHPFREKLTKALVTIAVINALALLIMCP---SAVTLVTRREEH--- 187  
 LV +A+ER +I+P K++ +A + I +W +A++ P +++ V + H  
 Sbjct 132 LVVLVALERHQILNTPGWKPSISQAYLGIVLIVIACTVLSPLFLANSILENVPHKNSKA 191

Query 188 -HFVMDARNRSYPLSCWEAMPEKGMRRVYITVLFHSIYALPLALIVMYARIARLKQA 246  
 F+ D C E+WP R +YTT L Y PL I+V YARI R+L+  
 Sbjct 192 LEFLADK-----VVCESWPLAHRTITVTLFLLPQYCLPLGFIIVCTARIYRLQRO 244

Query 247 PGPAQGEAADPRASRRARVRVHMLVVALPFTLSWPLMALALLIDYQQLSAPQLHLV 306  
 G + RA + +V +LV++ + F + WLPL L D+ + P H  
 Sbjct 245 GRVPHKGYSL--RAGHK-QVNVLVVMVAVFVLMPLHIVFNSLEDWHEATIPICHGN 301

Query 307 TVYAPFAHMLAFNSSANPIIYGFNENPERGQA 342  
 + F H LA ++ NP IYG+ N NP++ +A  
 Sbjct 302 LI--FLVCHLLAASCTCVNFIYGLNPLNPKKEKA 335

>emb|CAG46748.1| **[G]** PPYR1 (Homo sapiens)  
 Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 143 bits (361), Expect = 9e-34, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 166/336 (49%), Gaps = 19/336 (5%)

Query 14 PLSQMTNTTEATPATLNTSSYYQHTSPVAAMFVAYALIFLLCMVGNLTVCFVILKNRH 73  
P S G N T P S + Q + V + +Y++ ++ +GN + + + +  
Sbjct 12 PHSQGNENRSLKPTGTFYPSRSHQQSDVWVYVTSYTSRTYVQVIGLCLCMCVTVKRE 71

Query 74 MHTVTMIFILNLAVDLLGVICMPTTVLVDNLTIGWPFQATCKMSGLVQMSVSASVPT 133  
VTD + I NLA SD ++ C P T V ++ W P CDS +0 MEV S +  
Sbjct 72 KANVTNLLIANLAPSDFLMCLLCQPLTAVTIDMYIGFETLCKMSAPIQCMSVTVSILS 131

Query 134 LVAIAVERFCIVHPFREKLTLKALVTIAVINALALLIMCP--SAVTLTVTREH-- 187  
LV +A+ER + I++P K ++ +A + I +IW +A ++ P +++ V + H  
Sbjct 132 LVLVALERHQLIINPTQWKPISQAYLIGLIVIAICVLSPLFANSLLENVPHKNSKA 191

Query 188 -HFVVDARNRSYPLYSCEWAEPMKQNRVTVTLFVSHIYAPLALVVMYARIARLQQA 246  
P + D + C A WP R +YTT L Y PL I+V YARI F L  
Sbjct 192 LEFLADK-----VVCETSWPLAHERITVYTLFLLQYCLPLGFIYCVARIYRCLQR 244

Query 247 PGPAFGGEAADPRASRRARVVMHLMVALFPTLSWPLMALLLLIDYQLSAPQHLHV 306  
G + RA + +V +LW++ + F +WLPL L D+ + P R  
Sbjct 245 GRVPHKGTYSL--RAGHK-QVNVLVVMVAVLNLFLVFNLSDEMHHEAIPICGN 301

Query 307 TVYAFPFAMHIAFFNSSANIIYGFNFNFRGQA 342  
F H LA ++ N FYG+ N NF++ +A  
Sbjct 302 LI--FLVCLILMASTVCNMFPIGFLTNKKEIKA 335

-gb|BAW54325.1| **C** tachykinin receptor 2, isoform CRA\_b [Homo sapiens]  
Length=399

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 142 bits (357), Expect = 3e-33, Method: Compositional matrix adjust.  
Identities = 117/409 (28%), Positives = 184/409 (44%), Gaps = 26/409 (6%)

Query 21 NTEATPATLNTSSYYQHTSPVAAMFVAYALIFLLCMVGNLTVCFVILKNRHHTVTNM 80  
N + P +N T + + S A++ AY + L+ +GN +V +I+L +R M TVTN  
Sbjct 11 NISSGPGSHTTGTAFSPMSQALMATAIYALVLAVTNGAIVIMILAHRRNRTVTNY 70

Query 81 FILNLAVSDLLGVICMPTTVLVDNLTIGWPFQATCKMSGLVQMSVSASVPTLVAIVE 140  
FI+NLA++DL + F +V + N F P A C L ++ S+++ ALA +  
Sbjct 71 FIVNALADLCMAFNAAFNPFYASNNIWFGRACFYQNLFPTITAMFYSYNTAIAAD 130

Query 141 R-FRCIVHPFREKLTLKALVTIAVINALALLIMCPSAVTLTVTREHHPVDARNRSYP 199  
R + IVHFP +L+ IA IW +AL + P TVT ++  
Sbjct 131 RQYMAIVHPQRLASPTKAVIAGIWLVALALASPOCFYSTVTMDQ-----GA 178

Query 200 LYSCEWAEPMKQNR--VYTVLFSHIYAPLALVVMYARIARLQQAAPGAPGEEA 256  
C AMPE ++ +Y V+ +Y PL++ V Y+ I L + P G +A  
Sbjct 179 ATKCVAMREDSGGKTLILYHVALIYTLPLAVMVAVSIGLTHRAVTP--GROM 235

Query 257 --ADPRASRRARVVMHLMVALFPTLSWPLMALLLLIDYQLSAPQHLVTVYAFPPA 314  
A+ R + + + V +V L F + N P +L+ +L + + VY F  
Sbjct 236 HGANLRLHQAQKKPVKTMVLVLTFAICMLPYHLYFILSGPQEDYICHKFIQOVYALF-- 294

Query 315 HILAFNSSANIIYGFNFNFRGQAAPRRLCPRPSGSHKEAYSERPGGLHRRVFP 374  
WLA ++ NPIIY N FR GP+ AFR CP + + + P L RV  
Sbjct 295 -WLASSSTHNPITYCLNHRFRSGPLAFRC--CPWVTPTEKDKLELTSTSTVRNR 351

Query 375 VVRPSDGLSPESGSPGAPRPGRLPLNRGVARHGLPREGPGCSHLPL 423  
P + + + P + + G G P +L+ +  
Sbjct 352 CHTKETLPMAGDTAPSEATSGEAGR- QDGSGLWFGYGLLAPTKTHVEI 398

-gb|AAH96842.1| **C** Tachykinin receptor 2 [Homo sapiens]  
Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 140 bits (353), Expect = 9e-33, Method: Compositional matrix adjust.  
Identities = 115/408 (28%), Positives = 182/408 (44%), Gaps = 25/408 (6%)

Query 21 NTEATPATLNTSSYYQHTSPVAAMFVAYALIFLLCMVGNLTVCFVILKNRHHTVTNM 80  
N + P +N T + + S A++ AY + L+ +GN +V +I+L +R M TVTN  
Sbjct 11 NISSGPGSHTTGTAFSPMSQALMATAIYALVLAVTNGAIVIMILAHRRNRTVTNY 70

Query 81 FILNLAVSDLLGVICMPTTVLVDNLTIGWPFQATCKMSGLVQMSVSASVPTLVAIVE 140  
FI+NLA++DL + F +V + N F P A C L ++ S+++ ALA +  
Sbjct 71 FIVNALADLCMAFNAAFNPFYASNNIWFGRACFYQNLFPTITAMFYSYNTAIAAD 130

Query 141 RFRICIVHPFREKLTLKALVTIAVINALALLIMCPSAVTLTVTREHHPVDARNRSYPL 200  
R + IVHFP +L+ IA IW +AL + P TVT ++  
Sbjct 131 RYMAIVHPQRLASPTKAVIAGIWLVALALASPOCFYSTVTMDQ-----GA 178

Query 201 YSCHEWAEPMKQNR--VYTVLFSHIYAPLALVVMYARIARLQQAAPGAPGEEA- 256  
C AMPE ++ +Y V+ +Y PL++ V Y+ I L + P G +A  
Sbjct 179 TKCVAMREDSGGKTLILYHVALIYTLPLAVMVAVSIGLTHRAVTP--GROM 235

Query 257 --ADPRASRRARVVMHLMVALFPTLSWPLMALLLLIDYQLSAPQHLVTVYAFPPA 315  
A+ R + + + V +V L F + N P +L+ +L + + VY F  
Sbjct 236 HGANLRLHQAQKKPVKTMVLVLTFAICMLPYHLYFILSGPQEDYICHKFIQOVYALF-- 293

Query 316 WILAFNSSANIIYGFNFNFRGQAAPRRLCPRPSGSHKEAYSERPGGLHRRVFP 375  
WLA ++ NPIIY N FR GP+ AFR CP + + + L RV  
Sbjct 294 -WLASSSTHNPITYCLNHRFRSGPLAFRC--CPWVTPTEKDKLELTSTSTVRNR 351

Query 376 VVRPSDGLSPESGSPGAPRPGRLPLNRGVARHGLPREGPGCSHLPL 423  
P + + + P + + G G P +L+ +  
Sbjct 352 HTKETLPMAGDTAPSEATSGEAGR- QDGSGLWFGYGLLAPTKTHVEI 398

-gb|AAB20304.1| substance K receptor, SK receptor [human, Peptide, 398 aa]  
Length=398

Score = 139 bits (350), Expect = 2e-32, Method: Compositional matrix adjust.  
Identities = 116/402 (28%), Positives = 181/402 (45%), Gaps = 36/402 (8%)

```
Query 21 NTEATPATNLTFSSVQHTSPVAAMFIVAYALFLLCHVGNATLVCFLVKNRHMVTVM 80
      N + P + N T + + S A + A + L + GN + V + I + L + R M TVTN
Sbjct 11 NISSGPESNTTGTATSPMPSQWLALMATAVLALVAVTGNIAIWIILAKHRMRTVNY 70

Query 81 FILNLAVSDLLVGLVCMPTTLDVNLITGMFPDFDNATCKMGLVQGMSSVSASVPTLVAIAE 140
      FI + NL + A + DL + P V W F A C L + S + + + AIA +
      FIVNLALDLKALNAAPFVYASHNIMWYRACFCYFQNIPIITAMFVYSMTAJAAD 130

Query 141 RPRCIVHPFREKLITRKALVTIATINALALLIMPASAVTLTVTRESHHFVMDARNRSYPL 200
      R + IVRFP + I + I + W L F + WLP + L + + VY F
Sbjct 131 RYMAIVHPFQRLSPASTKAVIAGINLVALALASQCFYSTVTMDQ -----GA 178

Query 201 YSCWEAMPEKGMRR--VYITVLFSHIYAPLALIVMYARIARKLQAPGAPGAGEA- 256
      C AMPE + + V V + + IV PLA + + V + I L + P G + A
Sbjct 179 TKCVVAMPDESQGTLLLYHLVIALYVLPFLAVMFVAISVIGLTLMRRAPV---GHCAG 235

Query 257 -ADPRASRRRARVHMLVMVALFFTLSPWLWALLLIDYQGLSAPQLHLVTVPYFPAH 315
      A + E + + + + V + L F + WLP + L + + VY F
Sbjct 236 GANLRHLQAKKFKFVMTVLVLTFAICMLPYHLVILFSGQEDYCHKFIQOVLALF- 293

Query 316 WLAFPNSSANPIIYGYFNMFPRGQFAARLRCPRPSGSHKEAYSERPGGLHREVFVW 375
      WLA + + NPIIT N FR GP+ AFR CP + + + + P L RV
Sbjct 294 WLAMSTMYNPIIYCCLNHRFSGRFLAPRC-CPWVTPTKEDKLELTPTSLSTRVNR 351

Query 376 VRPDSGLPSESQSGAPGRGLRPLGNRAHAGLPRGPG 417
      + + PS + + G H P + G G
Sbjct 352 HTKETPLMAGGTAPSEAT-----GSEAGH-----PQDSSG 381
```

-prf|2118221A cholecystokinin A receptor  
Length=428

Score = 137 bits (346), Expect = 6e-32, Method: Compositional matrix adjust.  
Identities = 107/353 (30%), Positives = 170/353 (48%), Gaps = 61/353 (17%)

```
Query 44 AMFIVAYALFLLCHVGNATLVCFLVKNRHMVTVMFILNLAVSDLLVGLVCMPTTLDV 103
      A + I + YLIFLL + +GRTIV + + + + N TVTN+P+L+LAVSDLA+ +PCNP L+
Sbjct 42 AVQILVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 101

Query 104 NLITGWPWFNATCKMGLVQGMSSVSASVPTLVAIAIEPRFCIVHPFREKL--TLRKALVT 161
      NI + + P + A CK + + G SVS F LVAI+ER- I P + + T AL
Sbjct 102 NLLKQIPGSAVCKTITTYFMGTSVSVSTFNLVAISLERYGAIKCPLOSVMQTSXHALKV 161

Query 162 IAVIALALLIMPASAVTLTVTRESHHFVMDARNRSYPLSCHEAMPEKGMRRVYITVLF 221
      IA N L+ IM P + + + + N + C P M + + + T L
Sbjct 162 IAAVLCISPTIMTPYPI-----YSLVPPFTKMNQTNMRCRLLPNVQVQSWHTPL 214

Query 222 SHIYALPLALIVMYARIARKLQCA-----PGAPAGE EAAD----- 258
      +L L + G P Y Y G + E L
Sbjct 215 LILFLIPGVNVMYAIASLELYOGIKFEASQKSAKKEKPTSTSGKGYSDGQYLOKT 274

Query 259 -----PRASRRRA-----RVHMLVMVALFFTLSPWLWALL 291
      RA+R+ RV+ M++++ P L W+P+++
Sbjct 275 RPPKLELRQLSTGSSSRANRIRSNSSAANTMAKXKRVIRMLIVVLFCLMCPMIFSA 334

Query 292 LIDYQGLSAPQLHLVTVPYFPAHILAFPNSSANPIIYGYFNMFPRGQFAF 344
      Y SA + + + P L + + S PLIV + N+ FR GP+ A F
Sbjct 335 WRAYDTASAE--RLSGTPIFILL+GYISSCNVPIIYCFMNRKRLGFWATF 385
```

-gb|AAL26488.1|AF411117\_1 G protein-coupled receptor [Homo sapiens]  
Length=455

Score = 135 bits (340), Expect = 3e-31, Method: Compositional matrix adjust.  
Identities = 85/296 (28%), Positives = 137/296 (46%), Gaps = 45/296 (15%)

```
Query 52 LIFLLCMVGNATLVCFLVKNRHMVTVMFILNLAVSDLLVGLVCMPTTLDVNLITGMFP 111
      LIF L + GN LV + + + M TVTN+FI +LA+SDLL+ PCP T+ N+ W
Sbjct 116 LIFLAFALGNALVYFVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 175

Query 112 DNATCKMGLVQGMSSVSASVPTLVAIAIEPRFCIVHPFREK--LITRKALVTIATINAL 169
      CKM VQ + V + T+ IAVER + +VHPF+ K T R+A + V+W+A
Sbjct 176 GAFICGMVFPVQSTAVVTETLTMTCTIAVERHQGLVHPFMKMQYTNRRATNLGVMLVA 235

Query 170 LLIMCP--SAVTLTVTRESHHFMDARNRSYPLSCHEAMPEKGMRRVYITVLFSHIYLA 227
      + + P L + + + P + + C E W + + + VTT + S
Sbjct 236 VIVGSPHMHVQGLIE--KYDFLYKEH-----ICLLKEKETSVPVHQKTYITFLSSSSC 287

Query 228 PLALIVMYARIARKLQAPGAPGAGEAADPRASRRRARVHMLVMVALFFTLSPWLW 287
      P + + + R V + W + V F + W P
Sbjct 288 LLW-----KKRAVINMTVVALFAVCAPFH 314

Query 288 ALLLLIDYQGLSAPQLHLVTVPYFPAHILAFPNSSANPIIYGYFNMFPRGQFAA 343
      + + I + Y + + F + + P NS NPI+Y + NENF+ + A
Sbjct 315 VVRMIEYSNFEKYDDVTIKMFAIVQIGFNSNICNPVYAFMNFKKNVLSA 370
```

-dbj|BAD92474.1| G neuropeptide Y receptor Y1 variant [Homo sapiens]  
Length=262

GENE ID: 4886 NPY1R | neuropeptide Y receptor Y1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 127 bits (318), Expect = 9e-29, Method: Compositional matrix adjust.  
Identities = 79/206 (38%), Positives = 116/206 (56%), Gaps = 7/206 (3%)

```
Query 41 PVAMETVA--YALIFLLCMVGNATLVCFLVKNRHMVTVMFILNLAVSDLLVGLVCMFP 98
      P + + + GN + + + GN + I+L+ M TVTN+I+H+ SDLLV I C+ P
Sbjct 44 PLAMITFLALAYGALVILGVSQNALILIIILKOKEMRNVTILNLVLSFSDLLVAINCLP 103

Query 99 TTLVNLITGMFPDFNATCKMGLVQGMSSVSASVPTLVAIAIEPRFCIVHPFREKLITRKA 158
      T V L+ W F A CK+ + VQ + S+ + S+F+LV IAVER + I+P + R A
Sbjct 104 PTFTVITLMDHWVGRANCLNAPFVQCVSITVIFSLVLIAPERHQLIINPRGRFNRNHA 163
```

Query 159 LVTIAVINALLIMCPSAVILTITREE-HHFMVDARNRSYPLYSCHWEANPEKMMRVYT 217  
 V IAVIN LA+ P T E +DA Y C+ +P R VT  
 Sbjct 164 YGVIATVGLVAASSLFLIYQVWTFDPFQWTLIDYKDK--YVCFQPFSSDHSRLVYT 220

Query 218 TVLFSHYIAPLALIVVMYARIKKL 243  
 T+L Y PL I + Y + RKL  
 Sbjct 221 TLLLVQLVQPLGCFPIICYFKV-RKL 245

>gb|AA122552.1| **G** Tachykinin receptor 3 [Homo sapiens]  
 Length=465  
 GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 125 bits (315), Expect = 2e-28, Method: Compositional matrix adjust.  
 Identities = 100/386 (25%), Positives = 172/386 (44%), Gaps = 35/386 (9%)

Query 24 ATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCVGNLTVCPIVKRHHMTVTNMFIL 83  
 + P NLG + S A+ +AY + + +GN +V +I+L + M TVTN F+  
 Sbjct 68 SOPWNL--NQVQPSRIALMSAVYGVAVLGNLIVITLAKHMRVTVTNMFIL 125

Query 84 NLAVSDLLVIGFCMPTLNDLITQWFDNATCKMSGLVQGSMSVASVPTLVAIAVERFR 143  
 NLA SD + F + L + W F C+ +V AS+++ AIAR+R  
 Sbjct 126 NLAFSDASMAAFNLVNFVIALHSMYFGANYCRQNFPTITAVFASISMTAIAVDRYM 185

Query 144 CIVHPFREKLTLRKALVTIAVIALALLIMCPSAVILTITREEHHFMVDARNRSYPLYS- 202  
 I+ P + +L+ + I IW LA L+ P + + + P +  
 Sbjct 186 AIIDPLKRLSATATKIVIGSIWILAFLLAPQCLY-----SKTKVMPGRTL 232

Query 203 CHEANPEKMMR-VYTVLFSHYIAPLALIVVMYARIKKLQAPGAPGGEAAADPRA 261  
 C+ WPE Y + V PL ++ + Y + L P ++  
 Sbjct 233 CFVQWPEGPKQHFTHIIVITLVCFPLIMGITTYITVIGITLWGEIIGDTCYKHEQL 292

Query 262 SRRRARVHMLVMVAFPTLSMLPWLALLLIDYQGLSAPQLHVTVYAFPAHMLAFN 321  
 +R +VV M+ +V + F + WLP +L O ++ VY F WLA +  
 Sbjct 293 AKR--KVVMMIIVMTFAICWLFPHIYFILTITVQQLNRWKYIQVYLASF--NLAMS 348

Query 322 SANPIIYGYNFNRPRGQAPARLCP-----RPSGSHKEAYSERGGGLH 369  
 + NPIV N+ FR GP+ AF R CP + H S  
 Sbjct 349 TMYNPIIYCCLNKRFAGKRAF--RMCPIKVSYSDELELKTFRFNRQSSMYVTM 406

Query 370 RRVFVVFRPSDGLPESGSPSSGAPR 395  
 + VV P+D+ S PR  
 Sbjct 407 ESMTVFDPNDADTTRSSKKRKRATPR 432

>gb|AAB21706.1| **G** neurokinin-3 receptor; NK-3 receptor [Homo sapiens]  
 Length=465  
 GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 125 bits (314), Expect = 2e-28, Method: Compositional matrix adjust.  
 Identities = 100/386 (25%), Positives = 172/386 (44%), Gaps = 35/386 (9%)

Query 24 ATPATNLTFSSYQHTSPVAAMFIVAYALIFLLCVGNLTVCPIVKRHHMTVTNMFIL 83  
 + P NLG + S A+ +AY + + +GN +V +I+L + M TVTN F+  
 Sbjct 68 SOPWNL--NQVQPSRIALMSAVYGVAVLGNLIVITLAKHMRVTVTNMFIL 125

Query 84 NLAVSDLLVIGFCMPTLNDLITQWFDNATCKMSGLVQGSMSVASVPTLVAIAVERFR 143  
 NLA SD + F + L + W F C+ +V AS+++ AIAR+R  
 Sbjct 126 NLAFSDASMAAFNLVNFVIALHSMYFGANYCRQNFPTITAVFASISMTAIAVDRYM 185

Query 144 CIVHPFREKLTLRKALVTIAVIALALLIMCPSAVILTITREEHHFMVDARNRSYPLYS- 202  
 I+ P + +L+ + I IW LA L+ P + + + P +  
 Sbjct 186 AIIDPLKRLSATATKIVIGSIWILAFLLAPQCLY-----SKTKVMPGRTL 232

Query 203 CHEANPEKMMR-VYTVLFSHYIAPLALIVVMYARIKKLQAPGAPGGEAAADPRA 261  
 C+ WPE Y + V PL ++ + Y + L P ++  
 Sbjct 233 CFVQWPEGPKQHFTHIIVITLVCFPLIMGITTYITVIGITLWGEIIGDTCYKHEQL 292

Query 262 SRRRARVHMLVMVAFPTLSMLPWLALLLIDYQGLSAPQLHVTVYAFPAHMLAFN 321  
 +R +VV M+ +V + F + WLP +L O ++ VY F WLA +  
 Sbjct 293 AKR--KVVMMIIVMTFAICWLFPHIYFILTITVQQLNRWKYIQVYLASF--NLAMS 348

Query 322 SANPIIYGYNFNRPRGQAPARLCP-----RPSGSHKEAYSERGGGLH 369  
 + NPIV N+ FR GP+ AF R CP + H S  
 Sbjct 349 TMYNPIIYCCLNKRFAGKRAF--RMCPIKVSYSDELELKTFRFNRQSSMYVTM 406

Query 370 RRVFVVFRPSDGLPESGSPSSGAPR 395  
 + VV P+D+ S PR  
 Sbjct 407 ESMTVFDPNDADTTRSSKKRKRATPR 432

>emb|CAA46291.1| **G** neuropeptide K receptor [Homo sapiens]  
 Length=465  
 GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 125 bits (314), Expect = 3e-28, Method: Compositional matrix adjust.  
 Identities = 95/366 (25%), Positives = 164/366 (44%), Gaps = 33/366 (9%)

Query 44 AMFIVAYALIFLLCVGNLTVCPIVKRHHMTVTNMFILNLAVSDLLVIGFCMPTLVD 103  
 A+ + +V Y + +GN +V +I+L + M TVTN F+ NLA SD +  
 Sbjct 86 ALMSIATVGLVAASSLFLIYQVWTFDPFQWTLIDYKDK--YVCFQPFSSDHSRLVYT 145

Query 104 NLITQWFDNATCKMSGLVQGSMSVASVPTLVAIAVERFRFRCIVHPFREKLTLRKALVIA 163  
 L + W F C+ +V AS+++ AIAR+R I+ P + +L+ + I  
 Sbjct 146 ALHSEMYFGANYCRQNFPTITAVFASISMTAIAVDRYMAIIDPLKRLSATATKIVIG 205

Query 164 VIVIALALLIMCPSAVILTITREEHHFMVDARNRSYPLYS-CHEANPEKMMR-VYTVL 221  
 I+ P + +L+ + I IW LA L+ P + + + P +  
 Sbjct 206 SINILAFLLAPQCLY-----SKTKVMPGRTLQVWPEGPKQHFTHIIVIT 252

Query 222 SHIYIAPLALIVVMYARIKKLQAPGAPGGEAAADPRASRRARVHMLVMVAFPTL 281

Sbjct 253 +Y PL ++ + Y + L P ++ + ++R +VV N+++V + F + 310  
ILVYCFPLLIMGITTYITVIGITLWGGEIPGDCDKYHEQLKAKR--KVVNMIIIVVMTFAI

Query 282 SWLPLKALLLLIDYQGLSAPQLHLVTVYAPFAHMLAFNSSANPIIYGVFNENFRGQ 341  
WLP +L Q ++ VY F WLA ++ NPIIY N+ FR GP+

Sbjct 311 CWLPHYIYFILTAYIQQLNRWKYIQQVYLASF--WLAWSSTMYNPIIYCLNKRFRAGFK 368

Query 342 AAFARLCP-----RPSGSHKAYSERPQGLLHRRVFPVVRPSDGLPSESOP 389  
AF R CP + + H S + VV P+D+ S

Sbjct 369 RAF--RWCPFKVSSYDELELKTTRFPHNRQSSMYTVTRMESMTVVPDADTTRSSRK 426

Query 390 SSGAPR 395  
PR

Sbjct 427 KRATPR 432

>ref|NP\_001050.1| **G** tachykinin receptor 3 [Homo sapiens]

sp|P29371.1|NK3R\_HUMAN **G** RecName: Full=Neurokinin-K receptor; Short=NKR; AltName: Full=Neurokinin B receptor; AltName: Full=NK-3 receptor; Short=NK-3R; AltName: Full=Tachykinin receptor 3

gb|AA36366.1| **G** neurokinin-3 receptor

gb|AAR23926.1| **G** tachykinin receptor 3 [Homo sapiens]

gb|AAI21807.1| **G** Tachykinin receptor 3 [Homo sapiens]

gb|EAX06173.1| **G** tachykinin receptor 3 [Homo sapiens]

Length=465

GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
(Over 10 PubMed links)

Score = 125 bits (314), Expect = 3e-28, Method: Compositional matrix adjust.  
Identities = 95/366 (25%), Positives = 164/366 (44%), Gaps = 33/366 (9%)

Query 44 AMFIVAYALIFLLCHVGNTLVCPVLNRRHMTVWMPILNLAASDLGVPFCMPTFLVD 103  
A++ +Y ++ + +GR +V +L ++ M TVTN F++WLA SD + P +

Sbjct 86 ALMSIAYGVVAVAVGLNLIWIMILAHKRMRTVTVYVNLIAFSDASMAAFNTLVNFIY 145

Query 104 NLITGWPFNDATCKMSGLVQGSVSASVPTLVAIAVERPCIVHFFREKLTLEKALVITA 163  
L + N F C+ +V AS+++ ATAV+R+ I+ P +L+ + I +

Sbjct 146 AGRSEWFGANYCRFPQNFITAVFASITSMATAVCRIMALIDPLKPLSATATKIVIG 205

Query 164 VINALLALIMCPSAVTLVTRREHFMVDARNSSVPLYS-CWEAPKEGMR-VYTVLFI 221  
IW LA L+ + + + P + C+ WFE + Y ++

Sbjct 206 SIMILAFLLAFQCLY-----SKTKVMFGRTLCPVWPEGPKQHTFYHIIYI 252

Query 222 SHIYLAPLALIVVMYARIARKLCQAPGAGEAADPRASERARVVMVLVVALFPTL 281  
+Y PL ++ + Y + L P ++ + ++R +VV N+++V + F +

Sbjct 253 ILVYCFPLLIMGITTYITVIGITLWGGEIPGDCDKYHEQLKAKR--KVVNMIIIVVMTFAI 310

Query 282 SWLPLKALLLLIDYQGLSAPQLHLVTVYAPFAHMLAFNSSANPIIYGVFNENFRGQ 341  
WLP +L Q ++ VY F WLA ++ NPIIY N+ FR GP+

Sbjct 311 CWLPHYIYFILTAYIQQLNRWKYIQQVYLASF--WLAWSSTMYNPIIYCLNKRFRAGFK 368

Query 342 AAFARLCP-----RPSGSHKAYSERPQGLLHRRVFPVVRPSDGLPSESOP 389  
AF R CP + + H S + VV P+D+ S

Sbjct 369 RAF--RWCPFKVSSYDELELKTTRFPHNRQSSMYTVTRMESMTVVPDADTTRSSRK 426

Query 390 SSGAPR 395  
PR

Sbjct 427 KRATPR 432

gb|AAH95527.1| **G** TACR3 protein [Homo sapiens]

Length=464

GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
(Over 10 PubMed links)

Score = 124 bits (311), Expect = 7e-28, Method: Compositional matrix adjust.  
Identities = 100/386 (25%), Positives = 170/386 (44%), Gaps = 35/386 (9%)

Query 24 ATPATNLTSSYYQTSVPAAMFIVAYALIFLLCHVGNTLVCPVLNRRHMTVWMPIL 83  
+ P TNLIT + + S A + +AY ++ + +GN +V +L ++ M TVTN F++

Sbjct 67 SQPWNTLT--NQPVQPSRWIAPLASVGVVAVAVGLNLIWIMILAHKRMRTVTVYFI 124

Query 84 NLAASULLLVGIPMPTLVNLIWIMVUNATCKMSGLVQGSVSASVPTLVAIAVERFR 143  
NLA SD F P + L + W F C+ +V AS+++ IAVR+R

Sbjct 125 NLAASDASMAAFNTLVNFIWILALASRWGANVCYCFQNFPPITAVFASITSMATAVRYM 184

Query 144 CIVHFFREKLTLEKALVITAVIALLALIMCPSAVTLVTRREHFMVDARNSSVPLYS- 202  
I+ P +L+ + I +L+ + I +L+ + P

Sbjct 185 AIIDPLRPLSATATKIVIGISWILAFLLAFQCLY-----SKTKVMFGRTL 231

Query 203 CWEAPKEGMR-VYTVLFSHIYLAPLALIVVMYARIARKLCQAPGAGEAADPR 261  
C+ WFE C Y ++ +V PL ++ + Y + L P ++ +

Sbjct 232 CFVWPEGPKQHTFYHIIYVILVYCFPLLIMGITTYITVIGITLWGGEIPGDCDKYHEQLK 291

Query 262 SRRARVVMVLVVALFPTLSWLPLKALLLLIDYQGLSAPQLHLVTVYAPFAHMLAFN 321  
+R +V VV N+++V + F + WEP +L Q ++ VY F WLA +

Sbjct 292 AKR--KVVNMIIIVVMTFAICWLPHYIYFILTAYIQQLNRWKYIQQVYLASF--WLAWS 347

Query 322 SSANPIIYGVFNENFRGQAAAFARLCP-----RPSGSHKAYSERPQGLLH 369  
+ NPIIY N+ FR GP+ AF R CP + + H S

Sbjct 348 THYNPIIYCLNKRFRAGFKRAF--RWCPFKVSSYDELELKTTRFPHNRQSSMYTVTRM 405

Query 370 RRVFPVVRPSDGLPSESOPSSGAPR 395  
+ VV P+D+ S PR

Sbjct 406 ESMTVVPDADTTRSSRKRAATPR 431

sp|Q13585.1|MTIRL\_HUMAN **G** RecName: Full=Melatonin-related receptor; AltName: Full=G protein-coupled receptor 50; AltName: Full=H9

gb|AAC50614.1| **G** melatonin-related receptor

Length=613

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 123 bits (308), Expect = 1e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIFLLC-----MVGNTLVCFVLKRRHMTVTNNFILNLVSDLLVGICPMPTTLV 102
+I+ C ++GN+V V KN+ + N+P++L+V+D+L+I+ P L
Sbjct 28 IIFMFCAMVITIVDLIGNSVILAVTNKKLRNSGNI PVVLSVADMLVAIYPPLMLH 87

Query 103 DNLITGPFNDATCKMSGLVQMSVSASVPTLVAIAVERFRCI VHPFREK--LTLRKALV 160
I GN C+M G +G+SV S+F +VAIA+ R+ I H + + +R+
Sbjct 88 AMSIGDGLSGLQCGMVGITGLSVGSI PNIVAIINRYCI CHSLQYERIFSVMTCT 147

Query 161 TIATVIALALLIMCPSAVITLVTRREEHFMVDARNRSYPLYSCEAWPEKGMRRVYITVL 220
+ W + +L+ P+ T+ D R Y+C + +V+T +
Sbjct 148 YLVITWMTVLAVLPMNYIGTIE-----YDPRT----YTCIFNYLNPP--VPTVTI 192

Query 221 FSHIYALPLALIVMYARIARKLQAPGAPGGEAADPRASRRARVHMLVMVVALFFT 280
++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHVPFLLLIGVFCYVRIWTKVLAARDPA----GQNPQGLAEVRNFLTMTFVILLFA 247

Query 281 LSWLPLWALLLLIDYQGLSAQPLH-LVTVYAPFPAHIAFPNSSANPIIYGYPNENFRG 339
+ W P+ L+L+L+ +S ++ + + +A++A+PNS N+IYG NENFR
Sbjct 248 VCMCPINVLTVLV---AVSPKEMAGKIPNMLYLAAYFIAYPNSCLNAVITGLLENFRRE 304

Query 340 QQAARA 346
+ P A
Sbjct 305 YWTFIHA 311
```

>ref|NP\_004215.2|  G protein-coupled receptor 50 [Homo sapiens]  
Length=617

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 123 bits (308), Expect = 1e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIFLLC-----MVGNTLVCFVLKRRHMTVTNNFILNLVSDLLVGICPMPTTLV 102
+I+ C ++GN+V V KN+ + N+P++L+V+D+L+I+ P L
Sbjct 28 IIFMFCAMVITIVDLIGNSVILAVTNKKLRNSGNI PVVLSVADMLVAIYPPLMLH 87

Query 103 DNLITGPFNDATCKMSGLVQMSVSASVPTLVAIAVERFRCI VHPFREK--LTLRKALV 160
I GN C+M G +G+SV S+F +VAIA+ R+ I H + + +R+
Sbjct 88 AMSIGDGLSGLQCGMVGITGLSVGSI PNIVAIINRYCI CHSLQYERIFSVMTCT 147


Query 161 TIATVIALALLIMCPSAVITLVTRREEHFMVDARNRSYPLYSCEAWPEKGMRRVYITVL 220
+ W + +L+ P+ T+ D R Y+C + +V+T +
Sbjct 148 YLVITWMTVLAVLPMNYIGTIE-----YDPRT----YTCIFNYLNPP--VPTVTI 192

Query 221 FSHIYALPLALIVMYARIARKLQAPGAPGGEAADPRASRRARVHMLVMVVALFFT 280
++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHVPFLLLIGVFCYVRIWTKVLAARDPA----GQNPQGLAEVRNFLTMTFVILLFA 247

Query 281 LSWLPLWALLLLIDYQGLSAQPLH-LVTVYAPFPAHIAFPNSSANPIIYGYPNENFRG 339
+ W P+ L+L+L+ +S ++ + + +A++A+PNS N+IYG NENFR
Sbjct 248 VCMCPINVLTVLV---AVSPKEMAGKIPNMLYLAAYFIAYPNSCLNAVITGLLENFRRE 304

Query 340 QQAARA 346
+ P A
Sbjct 305 YWTFIHA 311
```

>gb|AAI03697.1|  GPR50 protein [Homo sapiens]

>gb|AAI05684.1|  GPR50 protein [Homo sapiens]  
Length=617

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIFLLC-----MVGNTLVCFVLKRRHMTVTNNFILNLVSDLLVGICPMPTTLV 102
+I+ C ++GN+V V KN+ + N+P++L+V+D+L+I+ P L
Sbjct 28 IIFMFCAMVITIVDLIGNSVILAVTNKKLRNSGNI PVVLSVADMLVAIYPPLMLH 87

Query 103 DNLITGPFNDATCKMSGLVQMSVSASVPTLVAIAVERFRCI VHPFREK--LTLRKALV 160
I GN C+M G +G+SV S+F +VAIA+ R+ I H + + +R+
Sbjct 88 AMSIGDGLSGLQCGMVGITGLSVGSI PNIVAIINRYCI CHSLQYERIFSVMTCT 147


Query 161 TIATVIALALLIMCPSAVITLVTRREEHFMVDARNRSYPLYSCEAWPEKGMRRVYITVL 220
+ W + +L+ P+ T+ D R Y+C + +V+T +
Sbjct 148 YLVITWMTVLAVLPMNYIGTIE-----YDPRT----YTCIFNYLNPP--VPTVTI 192

Query 221 FSHIYALPLALIVMYARIARKLQAPGAPGGEAADPRASRRARVHMLVMVVALFFT 280
++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHVPFLLLIGVFCYVRIWTKVLAARDPA----GQNPQGLAEVRNFLTMTFVILLFA 247

Query 281 LSWLPLWALLLLIDYQGLSAQPLH-LVTVYAPFPAHIAFPNSSANPIIYGYPNENFRG 339
+ W P+ L+L+L+ +S ++ + + +A++A+PNS N+IYG NENFR
Sbjct 248 VCMCPINVLTVLV---AVSPKEMAGKIPNMLYLAAYFIAYPNSCLNAVITGLLENFRRE 304

Query 340 QQAARA 346
+ P A
Sbjct 305 YWTFIHA 311
```

>gb|AAI05685.1|  G protein-coupled receptor 50 [Homo sapiens]

>gb|ABY7917.1|  G protein-coupled receptor 50 [Homo sapiens]  
Length=613

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
 Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

Query 52 LIFLLC-----MVGNTLVCFVLKRRHMTVTNFMILNVAESDLNGIFCMPTTLV 102  
 +IF+ C ++GN+V V KH+ + N+P+++L+V+D+LV I+ P L  
 Sbjct 28 IIFMFCANVITIVDGLGNSMVLAVTKKKLRNSGNI FVLSVADMVAIYPPMLML 87

Query 103 DNLITGWFNDATCKMSGLVQMSVSASVFTLVIAIAVERFCIVHPFREK--LTLRKALV 160  
 I GN C+M G + G+SV S+F +VAIA+ R+ I H + + ++R +  
 Sbjct 88 AMSIGDGLSOLQOCQMGVFTGLSVGSGI FNIVAIATINRYCIHSLQYERIFSVRNTCI 147

Query 161 TIAVIMALLIMCPSAVTLTVTREHHFPMVDARNRSYPLYSCEAWPEKMRVYTVTL 220  
 + W + +L+ +P+ T+ D R Y+C + V+T +  
 Sbjct 148 YLVITIMTVLAVLPHMYIGTIE-----YDPKT-----YTCIFNYLNNP--VFTVTI 192

Query 221 FSHIYLAPLALIVVMYIARLKCAQAPGAPGEEAADPRASRRARVVMIMVMVLFPT 280  
 ++ PL ++ Y RI K+ A PA +P R + ++ L P  
 Sbjct 193 VCIHFVPLLLIGVPCYRIWTKVLAARDFA----GQNPQDLAEVRNFTMFVILFLFA 247

Query 281 LSNPLMALLLIDYGLSAPQLH-LVTYAPFPANHLAFNNSANPIYGVFNENFRAG 339  
 + N P+ L +L+ +S ++ + + A+++FNS N +YGN NENFRE  
 Sbjct 248 VCMCPINVLTVL---AVSPKEMAGKIPNMVLAAYFIAYFNSCLNAVIGLLNENFRE 304

Query 340 QAAAFRA 346  
 + F A  
 Sbjct 305 YWTFIPA 311

>gb|EAW99402.1| **G** G protein-coupled receptor 50 [Homo sapiens]  
 Length=617

GENE ID: 8248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
 Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

Query 52 LIFLLC-----MVGNTLVCFVLKRRHMTVTNFMILNVAESDLNGIFCMPTTLV 102  
 +IF+ C ++GN+V V KH+ + N+P+++L+V+D+LV I+ P L  
 Sbjct 28 IIFMFCANVITIVDGLGNSMVLAVTKKKLRNSGNI FVLSVADMVAIYPPMLML 87

Query 103 DNLITGWFNDATCKMSGLVQMSVSASVFTLVIAIAVERFCIVHPFREK--LTLRKALV 160  
 I GN C+M G + G+SV S+F +VAIA+ R+ I H + + ++R +  
 Sbjct 88 AMSIGDGLSOLQOCQMGVFTGLSVGSGI FNIVAIATINRYCIHSLQYERIFSVRNTCI 147

Query 161 TIAVIMALLIMCPSAVTLTVTREHHFPMVDARNRSYPLYSCEAWPEKMRVYTVTL 220  
 + W + +L+ +P+ T+ D R Y+C + V+T +  
 Sbjct 148 YLVITIMTVLAVLPHMYIGTIE-----YDPKT-----YTCIFNYLNNP--VFTVTI 192

Query 221 FSHIYLAPLALIVVMYIARLKCAQAPGAPGEEAADPRASRRARVVMIMVMVLFPT 280  
 ++ PL ++ Y RI K+ A PA +P R + ++ L P  
 Sbjct 193 VCIHFVPLLLIGVPCYRIWTKVLAARDFA----GQNPQDLAEVRNFTMFVILFLFA 247

Query 281 LSNPLMALLLIDYGLSAPQLH-LVTYAPFPANHLAFNNSANPIYGVFNENFRAG 339  
 + N P+ L +L+ +S ++ + + A+++FNS N +YGN NENFRE  
 Sbjct 248 VCMCPINVLTVL---AVSPKEMAGKIPNMVLAAYFIAYFNSCLNAVIGLLNENFRE 304

Query 340 QAAAFRA 346  
 + F A  
 Sbjct 305 YWTFIPA 311

>ref|NP\_001718.1| **UG** bombesin-like receptor 3 [Homo sapiens]  
 sp|P32247.1|BR83 HUMAN **G** RecName: Full=Bombesin receptor subtype-3; Short=BRS-3  
 gb|AAA35604.1| **G** bombesin receptor subtype-3  
 emb|CAA54031.1| **G** uterine bombesin receptor [Homo sapiens]  
 emb|CAB10731.1| **G** bombesin-like receptor 3 [Homo sapiens]  
 gb|AAT79496.1| **G** bombesin-like receptor 3 [Homo sapiens]  
 gb|EAW88470.1| **G** bombesin-like receptor 3 [Homo sapiens]  
 Length=399

GENE ID: 680 BR83 | bombesin-like receptor 3 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
 Identities = 83/312 (26%), Positives = 151/312 (48%), Gaps = 17/312 (5%)

Query 48 VAYALIFLLCMGNTLVCFVLKRRHMTVTNFMILNVAESDLNGIFCMPTTLVNLIT 107  
 +YA+I ++GN++ + K + M TV N+P +LA DLL+ + C+P L  
 Sbjct 52 ITAVIISVGLNLAIKLVFFKTSQVYFNPIITSLAPGDLNLLLTCTVPDATHYAE 111

Query 108 GHPFNDATCKMSGLVQMSVSASVFTLVIAIAVERFCIVHPFREK--LRLKALVIATI 165  
 GN F CK+ + SV SVTTL ++R++ +V P + K V +  
 Sbjct 112 GNLFORIGCKVLSFIRLTVGVSVFTLTLSADRYKAVVKPLERQPSNAILKTCVKAGCV 171

Query 166 WALALLIMCPSAVTLTVT--REHHFPMVDARNRSYPLYSCEAWPEKMRVYTVLPSH 223  
 W +++ P A+ V R+ + M SYP+ +K ++ ++ + F  
 Sbjct 172 NTVSMIFALPEAIPSVRYTFRDPNKMFTFESCTSYPP-----SKLLQSHSLCLFLV 224

Query 224 IYLAPLALIVVMYIARLKCAQAPGAPGEEAADPRASRRARVVMIMVMVLFPTLW 283  
 F+ PL++I V Y+TAR L + +P R+ + + + + + F L W  
 Sbjct 225 FTIPLGSIISVYSLIARTIKYKSTINI PTEQSGHARKQIESKKIARTVLIVLVAIFALCW 284

Query 284 LPLMALLLIDYQGLSAPQLH-LVTYAPFPANHLAFNNSANPIYGVFNENFRAG 340  
 LP L L + + +H + F+ LAF NS NP + ++F+ + F  
 Sbjct 285 LPHNLLYLHSFTSQTVDPDSAMHFIFTI---FSKVLAFNSCNVFPALYVLSKSPQKH 341

Query 341 QAAFRARLCPRP 352  
 +A RP  
 Sbjct 342 KXQLPCCAKSRP 353

>emb|CAG46720.1| **G** DRD1 [Homo sapiens]



UG

LR1 |

**G**

18

**G**

GENE ID: 1812 DRD1 | dopamine receptor D1 [Homo sapiens]

(Over 100 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 146/320 (45%), Gaps = 36/320 (11%)

```
Query 60 GNTLVCFIVLKNRHHMT-VTNMFILNALVSDLLVGIFCMPTTLVDNLITGWFPDNATCKM 118
GNTLVCFIVLKNRHHMT-VTNMFILNALVSDLLVGIFCMPTTLVDNLITGWFPDNATCKM 118
Sbjct 40 GNTLVCAVIRFHLRSKVTNFFVISLAVSDLLVAVLWMPKAVARIAGFMPF-GSPCNI 98

Query 119 SGLVQMSVSASVFTLVAIAVERFCIVHPPR--EKLTLKALVTIAVWALLI-MCP 175
M +AS+ L I+V+R+ I PFR K+T + A + I+V W L+LI P
Sbjct 99 WVAFDIMCSTASILNLCVISDRYNAISSPFYRKMTKPAAFILISVAVTLVSLISFIP 158

Query 176 SAVTLVTREHHFMDVARNRSPYLYSCWAEKPMKRRVYTTVLFSHIYLAFLALIVVM 235
++ +A + + +C + + R + P+H+V
Sbjct 159 VQLSHWKAFTSPSGDNATSLRTDNC-----DSSLRTYAISSSVIYPIVAMIVT 213

Query 236 YARIAR-----KLQAPGAPAGGEEADPRAS----RRARVVMH 271
Y RI R K Q E + P + S +R +V+
Sbjct 214 YTRIRIAQKQIRRIALERAHAVKNCQTTTGNGKPVBCSQPSSFFKMSFKRETVKLKT 273

Query 272 LVNVALFTSLWPLNALLLLDYQGLAPQLHLVTYAPFAHWAFFNNSANPIYGY 331
L ++ F WLP + L ++ + Q + F W + NSS NPITY
Sbjct 274 LSVIMGVFCVCLLPFFILNLCILPFGSGGTOPPCIDSNFTDVPVWFGANSSINPIIYA- 332

Query 332 FNNFRGPGQAAPRA-RLCP 350
FN +FR+ P RLCP
Sbjct 333 FNADFRKAFSTLIGCTRLCP 352
```

>gb|AAK83235.1|AF34725.1 **G** G-protein-coupled receptor GPR54 [Homo sapiens]  
dbj|BA855446.1| **G** G protein-coupled receptor [Homo sapiens]  
gb|AAK33126.1| **G** putative G protein-coupled receptor [Homo sapiens]  
gb|AAP82929.1| **G** hypogonadotropin-1 [Homo sapiens]  
gb|BA69583.1| **G** KISS1 receptor [Homo sapiens]  
gb|AA140826.1| **G** KISS1 receptor [Homo sapiens]  
Length=398

GENE ID: 84634 KISS1R | KISS1 receptor [Homo sapiens] (Over 10 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 104/351 (29%), Positives = 168/351 (47%), Gaps = 29/351 (8%)

```
Query 9 PNSSWFLSQNQTTEATPATNLTFSSYQHTSPVAMPFIVAVLIFLLCHVNTLVCFIV 68
P+SF+P A N N + A - +A + LB +VGR+LV +++
Sbjct 9 PRASWGAANASGCPGCGA-NASDGVPSRAVDANVLPLFPAALMLLGLVNSLVIVY 67

Query 69 LKNRHHMTVTNMFILNALVSDLLVGIFCMPTTLVDNLITGWFPDNATCKMSGLVQMSVS 128
+++ M TVTN +I NLA +D+ + C+P T + + GW + CK +Q +SV
Sbjct 68 CRHKPMKVTNMFILNALVSDLLVGIFCMPTTLVDNLITGWFPDNATCKMSGLVQMSVS 127

Query 129 ASVFTLVAIAVERFCIVHPPR--EKLTLKALVTIAVWALLIMCPASVTLVTREE 186
A+ TL A+V+R+ A N N + T R AL +W + + SA L + R
ATCATLTMNSGVRYVTFPLRLALHRETPLRLALVSLHWGSAAV--SAFVLALR--
Sbjct 128 ATCATLTMNSGVRYVTFPLRLALHRETPLRLALVSLHWGSAAV--SAFVLALR-- 182

Query 187 HNFVMDARNRSPYLYSCWAEKPMKRRVYTTVLFSHIYLAFLALIVVMYARIARKLQ- 245
+ R Y C EA+P + + R + +YL FL YA + R L +
Sbjct 183 -----LSPGRAY-----CSEAFSRALERAFALYHLLALYLLPILATCACYANMLHGRV 234

Query 246 APGPAPG----GEEADPRASRRRVRVNMVLMVVALFTSLWPLNALLLLDYQGLSA 300
A PAP G+ A+ KA RA RAV + + V L F W P+ L L L G +
Sbjct 235 AVRFAPADSLAQGLVLR-RQAVDARNVSDLVAVVLLFANCKWQIQLFQIQAQAPGS 293

Query 301 FGLHLVTYAPF-FAHWAFFNNSANPIYGYFNNFRGPGQAAPRAFLRCP 350
Sbjct 294 WHPRSYAAYALKTNWCHNSYSNSALNPLLYAFLOSHPRQAFR----RVCP 339
```

>gb|BA69583.1| **G** dopamine receptor D1, isoform CRA\_a [Homo sapiens]  
Length=469

GENE ID: 1812 DRD1 | dopamine receptor D1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 146/320 (45%), Gaps = 36/320 (11%)

```
Query 60 GNTLVCFIVLKNRHHMT-VTNMFILNALVSDLLVGIFCMPTTLVDNLITGWFPDNATCKM 118
GNTLVCFIVLKNRHHMT-VTNMFILNALVSDLLVGIFCMPTTLVDNLITGWFPDNATCKM 118
Sbjct 63 GNTLVCAVIRFHLRSKVTNFFVISLAVSDLLVAVLWMPKAVARIAGFMPF-GSPCNI 121

Query 119 SGLVQMSVSASVFTLVAIAVERFCIVHPPR--EKLTLKALVTIAVWALLI-MCP 175
M +AS+ L I+V+R+ I PFR K+T + A + I+V W L+LI P
Sbjct 122 WVAFDIMCSTASILNLCVISDRYNAISSPFYRKMTKPAAFILISVAVTLVSLISFIP 181

Query 176 SAVTLVTREHHFMDVARNRSPYLYSCWAEKPMKRRVYTTVLFSHIYLAFLALIVVM 235
++ +A + + +C + + R Y + P+H+V
Sbjct 182 VQLSHWKAFTSPSGDNATSLRTDNC-----DSSLRTYAISSSVIYPIVAMIVT 236

Query 236 YARIAR-----KLQAPGAPAGGEEADPRAS----RRARVVMH 271
Y RI R K Q E + P + S +R +V+
Sbjct 237 YTRIRIAQKQIRRIALERAHAVKNCQTTTGNGKPVBCSQPSSFFKMSFKRETVKLKT 296

Query 272 LVNVALFTSLWPLNALLLLDYQGLAPQLHLVTYAPFAHWAFFNNSANPIYGY 331
L ++ F WLP + L ++ + Q + F W + NSS NPITY
Sbjct 297 LSVIMGVFCVCLLPFFILNLCILPFGSGGTOPPCIDSNFTDVPVWFGANSSINPIIYA- 355

Query 332 FNNFRGPGQAAPRA-RLCP 350
FN +FR+ P RLCP
Sbjct 356 FNADFRKAFSTLIGCTRLCP 375
```

>ref|NP\_000785.1| **U** **G** dopamine receptor D1 [Homo sapiens]  
sp|P21728.1|DRD1\_HUMAN **G** RecName: Full=D(1A) dopamine receptor



GENE ID: 84634 KISS1R | KISS1 receptor [Homo sapiens] (over 10 PubMed links)

Score = 122 bits (305), Expect = 3e-27, Method: Compositional matrix adjust.  
Identities = 104/351 (29%), Positives = 168/351 (47%), Gaps = 29/351 (8%)

```
Query 9 PNSSWPLSQNSHTTEATPATNLTFSSYQHTSPVAMPFIVAYALPLLWGVNLTVCPIV 68
      PN+SM N + A N + + A + + +A+ L+ +VGN+LV +++
Sbjct 9 PNASGAPANASCPGCGCA--NASDGPVPSPRAYDAMLVLPFFAALMLGLVNSLVIYVI 67

Query 69 LKRNHMTVTNMFILNLAVALDGLVPCMPPTLVNLTITGWFPNATCMKSLVGQMSVS 128
      ++ M TVTN +I NIA +D+ + C+P T + + +GM + + CK + +Q +SV
Sbjct 68 CRHGRMTVTNMFILNLAVALDGLVPCMPPTLVNLTITGWFPNATCMKSLVGQMSVS 127

Query 129 ASVPTLVIAIVERFRCIVHPFR--EKLTLKALVTIAVIMALALIMCPSAVTLVTREE 186
      A+ TL A+V+R+ V P R + + T R AL +W + + SA L + R
Sbjct 128 ATCATLTAMSVDRMTVTVPFLALALRRTPLALAVLSLWGSAAV--SAPVIALAR-- 182

Query 187 HHFVVDARNRSPYLYSCWEAWPEKGRMVRVTVLFSHIYLAFLALIVMYARIKLCQ- 245
      + R+Y C EA+P + + R + + +VL PL +A + R L +
Sbjct 183 ----LSPGPRAY----CSEAFPSRALERAPALYMLLALTLPLATCACTAAMLRLGRV 234

Query 246 APGPAGG----GSEADPRASRRRARVHMLVWALPFTLSLPLWALLLLIDYQGLSA 300
      A PAP + + + R+ R+ R+ V L F W P L +L L G S +
Sbjct 235 AVRFAPADSLAQGVLR--RAGAVRSGRLVAAVLLFAACWGPQLFLVLQALSPAGS 293

Query 301 PQLHLTVIYAPP--PAHMLAFNNSANPIIYGFNFNFRGQPAARFRLCP 350
      +A +A ++ NS+ NP+Y + + +FR+ F+ R+CP
Sbjct 294 WHFRSYAAALKYATKMSYNSALNPLLYAFGLSGHFRQAFR----RVCP 339
```

>prf|1614340A dopamine receptor D1  
Length=446

Score = 120 bits (302), Expect = 6e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 145/320 (45%), Gaps = 36/320 (11%)

```
Query 60 GNTLVCPIVLKRNHMTVTNMFILNLAVALDGLVPCMPPTLVNLTITGWFPNATCMK 118
      GNTLVC + + + RH+ + VTN F++LAVSDLLV + MP V + WFP + C +
Sbjct 40 GNTLVCVAIVRPHRLSKVTNPFVLSLAVSDLLVAVLWVMPKVAEIAAGWFP--GSPCNI 98

Query 119 SGLVQMSVSASVPTLVIAIVERFRCIVHPFR--EKLTLKALVTIAVIMALALI-MCP 175
      +M +AS+ + +I+V R+ I PFR K+T + A +I+V M L+L+I P
Sbjct 99 WVAIFADCTASLNLGLVIVNRYWALSPGFRVETNTPKAFILISVAMTLGVLSIPF 158

Query 176 SAVTLVTIYRERHMPVDARNRSPYLYSCWEAWPEKGRMVRVTVLFSHIYLAFLALIVM 235
      ++ +A + + +C + + R+Y L + P+A++ +V
Sbjct 159 VQLSMHRAKPTSPSDGNATSLAETIDNC----DSSLRTVLSISSVISFYIVAINIVT 213

Query 236 YARIAR-----KLCAQGPAPGGEAADPRAS-----RRARVVMH 271
      Y RI R + + + K K Q E + P +S +R + +V+
Sbjct 214 YTRIYIAQKIRRIALLERAAVHAKNCTTTGNGKLVCEQSPSSFMSFRKRTVKLT 273

Query 272 LVMVAFPLTSLNPLMALALLIDYQGLSAQGLHVTIYVAPPFANMLFNSSANPIIYGV 331
      L + + + + WLP Q + F M + NSG NPIY
Sbjct 274 LSVINGVPCVCMPLFPIILNCILPFCSSGETQPCIDSNTPFVVFVFGWANSNLSIYI- 332

Query 332 FNFNFRGQPAARFRLCP 350
      FN +FR+ P RLCF
Sbjct 333 FNADEFKAPSTLLGLYRLCP 352
```

>dbj|BA036078.1| **G** unnamed protein product [Homo sapiens]  
Length=370

GENE ID: 2834 PRLHR | prolactin releasing hormone receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 117 bits (294), Expect = 5e-26, Method: Compositional matrix adjust.  
Identities = 100/305 (32%), Positives = 153/305 (50%), Gaps = 25/305 (8%)

```
Query 60 GNTLVCPIVLKRNHMTVTNMFILNLAVALDGLVPCMPPTLVNLTITGWFPNATCMK 118
      GN L + + + + E + VTN + C HLA+SD+ + + C+P L + GM F + C +
Sbjct 77 GNCLLVLVIAVERLHNVNLLIGNIALSDVIMCTACVPLTAYAFERHGMVFGGLCHL 136

Query 119 SGLVQMSVSASVPTLVIAIVERFRCIVHPFREKLTLKALVTIAVIMALALIMCPSAV 178
      +Q ++V SVPTL IAV+R+ +VHP R ++LR + + IWA+ ++ P+AV
Sbjct 137 VFFLQPVTVYVSVPTLTIIAIVRVVVLVHPLRRKISRLSAYAVLAWLSAVLAPAAV 196

Query 179 TLTVTRESHHMPVDARNRSPYLYSCWEAW--PEKGRMVRVTVLFSHIYLAFLALIVMYA 237
      + + + + + C E W + + R+Y L + YL PL + + + Y
Sbjct 197 -----RTHVELKPHVDRL--CEEFMSGSEQRQLTAWGLLLVTLLEPLLILLSYV 246

Query 238 RIARKLCAQAPGAGGGEAADPRASRRRARVHMLVWALPFTLSLPLWALLLLIDYQ 297
      R+ KL P + AD +RRR +LV+V + P +WLP LL D
Sbjct 247 RVSVKLRNVVPGCVTQSQADWDARRRRRTFC--LLVVVVVFAVCLVHVNLRDLDP 305

Query 298 LSAQQLHLTVIYAPP----PAHMLAFNNSANPIIYGFNFNFRGQPAARFRLCP 353
      H + YAP RWA ++ NP IY + + +FR + + A PR
Sbjct 306 -----HAIQYAPGLVQLLCLWMSACNTPYIARWEDSPREELKLLVAN--PKKI 357

Query 354 GSHKE 358
      H +
Sbjct 358 APIGQ 362
```

>ref|NP\_001041.1| **G** somatostatin receptor 2 [Homo sapiens]  
13 more sequence titles

sp|P30874.1|SSR2\_HUMAN **G** RecName: Full=Somatostatin receptor type 2; AltName: Full=SSR2;  
AltName: Full=SRP-1  
gb|AA042809.1|AF184174.1 **G** somatostatin receptor 2A [Homo sapiens]  
gb|AAAS8248.1| **G** somatostatin receptor isoform 2  
gb|AAH19610.1| **G** Somatostatin receptor 2 [Homo sapiens]  
dbj|BAC06126.1| **G** seven transmembrane helix receptor [Homo sapiens]

gb|AA092064.1| **G** somatostatin receptor 2 [Homo sapiens]  
 gb|AAV38729.1| **G** somatostatin receptor 2 [Homo sapiens]  
 gb|AAH59495.1| **G** Somatostatin receptor 2 [Homo sapiens]  
 gb|EAM89112.1| **G** somatostatin receptor 2, isoform CRA\_b [Homo sapiens]  
 dbj|BAF83434.1| **G** unnamed protein product [Homo sapiens]  
 Length=369  
 GENE ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 117 bits (293), Expect = 8e-26, Method: Compositional matrix adjust.  
 Identities = 98/376 (26%), Positives = 170/376 (45%), Gaps = 44/376 (11%)  
 Query 1 MESEPGQPNIS--SNPLSQNGTNTATPATNLTFSSYYQHTSPVAAMPIVAYALIFLLCM 58  
 M EP ++ S P NG: +T +N T YY TS FI LC  
 Sbjct 3 MADPLNGQSHWLSISFPDLNGS-VVSTVTCGQ-EPYVLTGNSALVITPVVVCIGLCL- 59  
 Query 59 VNTLVCFVLKGRHMHVTVMFILNLAVSDLLVGIPCMPTTLVDNLITGWFPFDNATCKM 118  
 GNTLV ++ +L M TVTN++ILMLA++D L + +P N WPF A C++  
 Sbjct 60 -GNTLVVYILRYAKMTKTIITNIIILMLAIDELF-MGLPLFLAMQVALVHMPFGKALCRV 117  
 Query 119 SGLVQGSVSASVFTLVAIAVERPRCIHVHPFREKLTLR--KALVTIAIVMALALLIMCP 175  
 V G++ S+P L +++R+ +VHP + R ++T+AV M ++L++ P  
 Sbjct 118 VMTVDGINQFTSIFCLTVMSIDRYLAVVHPKISAKWRPRFRATMTMAV-MGVSLVLIP 176  
 Query 176 SAVTLVTREHHFPMVDARNRSPYLSCHWAEPEKMRVVTTLPSHI--YLAFLALIV 233  
 R + R+ SC WP + + + + + I +L PL +I  
 Sbjct 177 IMI-----YAGLSQNGWRSSCTINNPGESGANYTGTPIYITPLGLFLVLTIC 225  
 Query 234 VMYARIARKLCQAPGAPGGEAADPRASRRRARVVHMLVWALFPTLWPLWALLLLI 293  
 + Y I K+ G + + +V M + +V P WLP + +  
 Sbjct 226 LCTYLFIIRK-----KSGTIRVGSSKRRKSEKKVTRMVSIVVAVFPCWLPFY--IP 275  
 Query 294 DYQGLS----APQLHLVTYAPFFAHKLAFPNSSANPIIYGYPNENFRGQAAF-RAR 347  
 ++S +L F F L + NS ANP+V + ++NP+ PQ  
 Sbjct 276 NVSSVGSMAISPTALKM-----PQVVVLTYSANCAPIFLAFLSNKSSKSPVCLLVK 331  
 Query 348 LCPKPSGKSHKAEVSER 363  
 + G ++ +  
 Sbjct 332 VSGTDGDRSSDKQDK 347

gb|AAA20828.1| **G** somatostatin receptor  
 Length=363  
 GENE ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 117 bits (293), Expect = 8e-26, Method: Compositional matrix adjust.  
 Identities = 94/312 (30%), Positives = 148/312 (47%), Gaps = 40/312 (12%)  
 Query 60 GNTLVCFVLKGRHMHVTVMFILNLAVSDLLVGIPCMPTTLVDNLITGWFPFDNATCKM 119  
 GNTLV ++ +L M TVTN++ILMLA+D L + +P N + WPF C++  
 Sbjct 57 GNTLVVYILRYAKMTKTIITNIIILMLAVDVLV-MGLPLFLATQNASFPWPGVLCRLV 115  
 Query 120 GLVQGSVSASVFTLVAIAVERPRCIHVHPFREKLTLRKALVTI--AVIALALLIMCPSA 177  
 + G++ SVF L ++V+R+ +VHP R + + A W L+L + P  
 Sbjct 116 MTLDGVNQFTSIFCLTVMSIDRYLAVVHPLSSAKWRPRFRVAKLASAAANVLSLNSLPL 175  
 Query 178 VTLVTREHHFPMVDARNRSPYLSCHWAEPE----KGMRRVYTVLPSHIVLALALI 232  
 V V +L +C +WPE + +YT VL + APL +I  
 Sbjct 176 VFADVQEGG-----TCNASWPEPVGLMGAVFIIYTVGLG--FFAPLVLVI 217  
 Query 233 VMYARIARKLCQAPGAPGGEAADPRASRRRARVVHMLVWALFPTLWPLWALLLL 292  
 + Y I K+ A G R R +V H++V L F WLP + +  
 Sbjct 218 CLCYLLIVVVK-----RAAGVGVCRRESER--KVTMRVLVVVLVFGACHLPFTTVN 270  
 Query 293 IDYQGLSAPQLHLVTYAPFFAHKLAFPNSSANPIIYGYPNENFRGQAAFRLCLRP 352  
 ++ PQ + + F L++ NS ANP++YG+ ++NFR+ PQ LC R  
 Sbjct 271 --NLAVLPQ-EPASAGLYPFFVILSYANSANFVLYGLSDNFRQSPQKV---LCRLK 323  
 Query 353 SGRSHKAEVSER 364  
 K+A + P  
 Sbjct 324 GSGAKDADATE 335

>ref|NP\_001044.1| **H****G** somatostatin receptor 5 [Homo sapiens]  
 sp|P35346.3|SSR5 HUMAN **G** RecName: Full=Somatostatin receptor type 5; AltName: Full=SSSR  
 db|BA04107.1| **G** fifth somatostatin receptor subtype [Homo sapiens]  
 gb|AA831822.1| **G** somatostatin receptor subtype SSTR5, SRIF receptor subtype SSTR5  
 [human, Pept1de, 364 aa]  
 gb|AAL88744.1| **G** somatostatin receptor subtype 5 [Homo sapiens]  
 gb|EAM5687.1| **G** somatostatin receptor 5 [Homo sapiens]  
 Length=364  
 GENE ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 117 bits (293), Expect = 9e-26, Method: Compositional matrix adjust.  
 Identities = 94/312 (30%), Positives = 148/312 (47%), Gaps = 40/312 (12%)  
 Query 60 GNTLVCFVLKGRHMHVTVMFILNLAVSDLLVGIPCMPTTLVDNLITGWFPFDNATCKM 119  
 GNTLV ++ +L M TVTN++ILMLA+D L + +P N + WPF C++  
 Sbjct 57 GNTLVVYILRYAKMTKTIITNIIILMLAVDVLV-MGLPLFLATQNASFPWPGVLCRLV 115  
 Query 120 GLVQGSVSASVFTLVAIAVERPRCIHVHPFREKLTLRKALVTI--AVIALALLIMCPSA 177  
 + G++ SVF L ++V+R+ +VHP R + + A W L+L + P  
 Sbjct 116 MTLDGVNQFTSIFCLTVMSIDRYLAVVHPLSSAKWRPRFRVAKLASAAANVLSLNSLPL 175  
 Query 178 VTLVTREHHFPMVDARNRSPYLSCHWAEPE----KGMRRVYTVLPSHIVLALALI 232  
 V V +L +C +WPE + +YT VL + APL +I  
 Sbjct 176 VFADVQEGG-----TCNASWPEPVGLMGAVFIIYTVGLG--FFAPLVLVI 217

Query 233 VVMYARIARKLQAPGAPGGEEAADPRASRRRRVHMLVHVALFPTLSMLPLWALLLL 270  
 + Y I K+ A G R S R +V M++V L P WLP + + + +  
 Sbjct 218 CLCYLIVVVKV----RAAGVRVGVCRASER--KVTRMVLVHVALFPTLWLLPPTVNI 292

Query 293 IDYQGLSAQHLVTVYAPFFAHWLAFFNSANPIIYGVFNFRGFGQAARLCPRP 352  
 + + + PO F L+ NS ANP+VQ+ ++NFR+ PO LC P  
 Sbjct 271 -NLAVALPO-EPASAGLYPFVVILSYANSANPVLVGLSDNFRQSPQK+---LCRLK 323

Query 353 GSGHKRAVSERP 364  
 K+ A + P  
 Sbjct 324 GSGAKDADATEP 335

>ref|NP\_004239.1| **[L]G** protein-coupled receptor 10 [Homo sapiens]  
 sp|P49683.2|PRLHR\_HUMAN **[G]** RecName: Full=Prolactin-releasing peptide receptor; Short=PrRr  
 receptor; Short=PrRrP; AltName: Full=G-protein coupled receptor  
 10; Short=hGR3  
 dbj|BA31159.1| **[G]** human prolactin-releasing peptide receptor [Homo sapiens]  
 8 more sequence titles

dbj|BAB83030.1| **[G]** prolactin releasing peptide receptor [Homo sapiens]  
 gb|AAH95539.1| **[G]** PRLHR protein [Homo sapiens]  
 gb|AAI01491.1| **[G]** PRLHR protein [Homo sapiens]  
 gb|AAI01493.1| **[G]** PRLHR protein [Homo sapiens]  
 gb|EAW9413.1| **[G]** prolactin releasing hormone receptor, isoform CRA\_a [Homo sapiens]  
 gb|EAW9414.1| **[G]** prolactin releasing hormone receptor, isoform CRA\_a [Homo sapiens]  
 gb|AB052422.1| **[G]** prolactin releasing hormone receptor [Homo sapiens]  
 dbj|BAF83150.1| **[G]** unnamed protein product [Homo sapiens]  
 Length=370

GENE ID: 2834 PRLHR | prolactin releasing hormone receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 117 bits (292), Expect = 9e-26, Method: Compositional matrix adjust.  
 Identities = 100/305 (32%), Positives = 152/305 (49%), Gaps = 25/305 (8%)

Query 60 GNTLVCFVLQNRHMTVTNMFILNLAVSDLLVGIFCMPTTLVDNLI-TGVPFDNATCM 118  
 GN L+ ++ + R +H VTN I NLA+SD+L+ C+P TL GN F C +  
 Sbjct 77 GNCILVILVAVKRLNMTVTNMFILNLAVSDLLVGIFCMPTTLVAYAFERGVGGI L 136

Query 119 SGLVQMSVSASVFTLVAIAVERFCRIVHPFREKLTLEKALVTIAVINALALLIMCP 178  
 + + + + + VFTL IAV+R+ +VHP R +L+L+ IALR+ + + P+AV  
 Sbjct 137 VFPLQPVTVVVSFTLITIAVORYVVLVHPRLRISLKLASAVLAIALSALVLA 196

Query 179 TLTVTREHHFMVDARNRSPLYSCHEAM-PEKGMRYVTTLVFSHIYLAPLALIVMYA 237  
 H + V+ + L C E W + + R+Y L VL PL +L+ + Y  
 Sbjct 197 -----HTYHVELKPHVDNL--CESFQSGERQQLYANGLLVTTLLPLVLLISV 246

Query 238 RIARKLQAPGAPGGEEAADPRASRRRRVHMLVHVALFPTLSMLPLWALLLLIDYQ 297  
 R+ K L+V+ + +R R +L+V+ + P +WLP L L D  
 Sbjct 247 RSVKLRNVPVPGCVQSQWDRARRRRTFC-LLVVVVVVFAVHLVFNLLRDLDP 305

Query 298 LSAPOHLHVTYVAPP---FAHMLAFNSANPIIYGVFNFRGFGQAARLCPRP 353  
 H + YAP HMLA ++ NP IY + ++FR + A PR  
 Sbjct 306 -----HAIDFYAVGLVQLLCHMLAMSSACYNPFIYAWLHDSFREELKLLVAM--PRKI 357

Query 354 GSHKE 358  
 H +  
 Sbjct 358 AHQO 362

>gb|AA24810.1|AF184174.2 **[G]** somatostatin receptor 2B [Homo sapiens]  
 gb|EAW9111.1| **[G]** somatostatin receptor 2, isoform CRA\_a [Homo sapiens]  
 Length=356

GENE ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 116 bits (291), Expect = 1e-25, Method: Compositional matrix adjust.  
 Identities = 97/353 (27%), Positives = 163/353 (46%), Gaps = 43/353 (12%)

Query 1 MBGEQSPQNS--SWPLSQNGTNTATPATNLTFSSYQHTSPVAAMFIVAYALPILCM 58  
 M EP ++ S P NG+ +T +N T YS PI I LC  
 Sbjct 3 MADEPLNGSHWLSIPFDLNGS-VVSTHNSNOT-EFYDLSNAVLTFIYFVVCIGLC- 59

Query 59 GNTLVCFVLQNRHMTVTNMFILNLAVSDLLVGIFCMPTTLVDNLI-TGVPFDNATCM 118  
 GNTLV +++L+ M T+TN++ILRLA++D L + +P + + WEP A C+  
 Sbjct 60 GNTLVILVILVAKMCTVTNMFILNLAVSDEL+MLGLPFLMAQVLAHVNHPFGALCV 117

Query 119 SGLVQMSVSASVFTLVAIAVERFCRIVHPFREKLTLE---KALVTIAVINALALLIMCP 175  
 V G+ S+P L +++R+ +VHP + R ++T+AV W +L+L+ P  
 Sbjct 118 VMTVDGINOFTSIFCLTVMSIDRYLAHVHPKISKAKWRPRATKAMTMAV-MGVSLVILP 176

Query 176 SAVTLVTREHHFMVDARNRSPLYSCHEAMPEKGMRYVTTLVFSHI--YLAPLALIV 233  
 + R+ SC WD + + + + I +L PL + I  
 Sbjct 177 IMI-----YGLRNSQWRSSCTINPFGESGAMYTGFPIITLILGPIVPLTIC 225

Query 234 VVMYARIARKLQAPGAPGGEEAADPRASRRRRVHMLVHVALFPTLSMLPLWALLLL 293  
 + Y I K+ A G R S R +V M++V L P WLP + + + +  
 Sbjct 226 LCLYLPILIKV-----KSSGIRGVSKRKKSEKVTMRVSVIYAVFICWLPFY----IF 275

Query 294 DYQGLS-----APOLHLVTVYAPFFAHWLAFFNSANPIIYGVFNFRGFG 341  
 + +S P L + F F L + NS ANP+Y + ++NP+ + PO  
 Sbjct 276 NVSSVMAISPTPALKGM-----PDFVVVLTYSANCPILITAFSLDNFKSPQ 324

>ref|NP\_658986.1| **[L]G** prokineticin receptor 2 [Homo sapiens]  
 sp|Q8WJ6.1|PKR2\_HUMAN **[G]** RecName: Full=Prokineticin receptor 2; Short=PK-R2; AltName:  
 Full=G-protein coupled receptor 73-like 1; AltName: Full=GPR73b;

AltName: Full=GPR2

gb|AA06126.1|AF506288.1 G prokineticin receptor 2 [Homo sapiens]  
dbj|BAC24022.1| G GPR2 [Homo sapiens]  
emb|CAI22379.1| G prokineticin receptor 2 [Homo sapiens]  
gb|AAI04960.1| G Prokineticin receptor 2 [Homo sapiens]  
gb|AAI04962.1| G Prokineticin receptor 2 [Homo sapiens]  
Length=384

GENE ID: 128674 PROKR2 | prokineticin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 116 bits (291), Expect = 1e-25, Method: Compositional matrix adjust.  
Identities = 98/373 (26%), Positives = 173/373 (46%), Gaps = 41/373 (10%)

Query 16 SQGNTTEATP-----ATNLTPS-SYQHTSPV-----AMPIVAYAL- 52  
+GQW NP TD A++L+P+ SY P+ AA ++ AJ  
Sbjct 3 AQWG-NTSPFTNPNPQDHASSLSPNFSYGDYDLPMDDEDMDTKRTTFFAAKIVIGIALA 61  
Query 53 -IFLLQVGNLTVCPIVLKRNHMTVTNMPILNLAVSDLLVGICPMTITVDNLIT-IGW 109  
I L+ C +GN + + + + + + TN+ I NLA+SD LV I C P + + + W  
Sbjct 62 GIMLVCGIGNFVIAALTRYKRLNLTNLLIANLAISDFLVAICCPFMDYVYVQGLSW 121  
Query 110 PFDNATCQMSGLVQMSVSASVFTLVAIAVERFRCTVHPFREKLTLRKALATIAVWALA 169  
+ C + + +S+ S L+AIAR+R+ IVP+ + + + A IA+M+ +  
Sbjct 122 EHGHLVCSNVYLR+TSLVYSTNALLAIAIDRYLAIVHPLKPMNVQTSFLIALVMWVS 181  
Query 170 LLIMCPASVTLTVTREETHHVMDARNRSYPLYSCEWAMP- EKGMRRVYTVFLSHIYLA 227  
+L+ PSA T E P+V + + + + C + WP + + + Y + F + +  
Sbjct 182 ILIAIPSAFYAT--ETVLTVKSGKPIK---CQIIMPVDDQLYKYSPLFPGVPEVG 234  
Query 228 PLALIVVMYARIARKLCOAPGAPGGERAADPRASRRRARVHMLVMAFLPFTLSMLPLN 287  
P+ + + YARI+R+L D E+ R+ +V M + + + A + L W P +  
Sbjct 235 PWTYTLVARIARELWPKAVPGFQTEQIRKRLCRKRLVLCILITA-VYLCAAPPY 292  
Query 288 ALLLLDIYQ-QLSAPQLALVTVYAPFAHMLAFNNSANPIIYGYPNFRFGQAPARA 346  
+ + + + + H + T AP +S NS R + + N + P +  
Sbjct 293 GFTIVRDFPFTVPVKEKHYLT--AFYVVECIAMNSMINTVCFVTVMNNTCKYFKQML 350  
Query 347 RLCPRPSGSHKEA 359  
P GS A  
Sbjct 351 HWRPGRSGSKSSA 363

>gb|BAI0422.1| G prokineticin receptor 2 [Homo sapiens]  
Length=811

GENE ID: 128674 PROKR2 | prokineticin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 116 bits (290), Expect = 2e-25, Method: Compositional matrix adjust.  
Identities = 85/324 (26%), Positives = 153/324 (47%), Gaps = 18/324 (5%)

Query 43 AMPIVAYAL--IFLLQVGNLTVCPIVLKRNHMTVTNMPILNLAVSDLLVGICPMTT 100  
AA ++ AL L+ C +GN + + + + + TN+ I NLA+SD LV I C P  
Sbjct 478 AAKIVIGIALAGIMVCGIGNFVIAALTRYKRLNLTNLLIANLAISDFLVAICCPFE 537  
Query 101 LVDNLIT--GWFDNATCQMSGLVQMSVSASVFTLVAIAVERFRCTVHPFREKLTLRKA 158  
+ + + W + C + + +S+ S L+AIAR+R+ IVP+ + + + A  
Sbjct 538 MDYVYVQGLSWEHGVLCASVNYLRTVSLVYSTNALLAIAIDRYLAIVHPLKPMNVQTA 597  
Query 159 LVTIAVNALALLIMCPASVTLTVTREETHHVMDARNRSYPLYSCEWAMP- EKGMRRVY 216  
IA+M+ + + + PSA T E P+V + + + + C + WP + + + Y  
Sbjct 598 SFILALVMMVSLIIAIPSAFYAT--ETVLTVKSGKPIK---CQIIMPVDDQLYKYSY 650  
Query 217 TTVLPSHIVLAPALIVVMYARIARKLCOAPGAPGGERAADPRASRRRARVHMLVMA 276  
+F + + + P+ + + YARI+R+L D E+ R+ +V M + + + A  
Sbjct 651 FLFIQVGFVPGVVTMTLCYARISRELWPKAVPGFQTEQIRKRLCRKRLVLCILITA 710  
Query 277 LPFTLSMLPLWALLLLID-YQISAPQLHLVTVYAPFAHMLAFNNSANPIIYGYPNFR 335  
+ L W P + + + + H + T AP + +S NS R + + N + P +  
Sbjct 711 --VYLCAAPPYGFTIVRDFPFTVPVKEKHYLT--AFYVVECIAMNSMINTVCFVTVMN 766  
Query 336 FRFGQAPARLRLCPRPSGSHKEA 359  
+ P+ P GS A  
Sbjct 767 TMKYFKRMMLHWRPGRSGSKSSA 790

>dbj|BAG36594.1| G unnamed protein product [Homo sapiens]  
Length=369

GENE ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 116 bits (290), Expect = 2e-25, Method: Compositional matrix adjust.  
Identities = 96/376 (25%), Positives = 172/376 (45%), Gaps = 44/376 (11%)

Query 1 MEQSESPQPNW--SWPLSQNGTNTKATPATNLTPSSYQHTSPVAMPIVAYALIFLLCM 58  
M EP + + S P NC+ + +T N+ T Y Y TS PI Y + + + +  
Sbjct 3 WDEPLNGSTWLSIIPDLNKS-VVSTNSQGT-EPYDLSNTAVLTFI-YPVVICGL 58  
Query 59 VGNLTVCPIVLKRNHMTVTNMPILNLAVSDLLVGICPMTITVDNLITGMPDNATCM 118  
GNLTW + +L+ M T TN+ILNLA+D L + +P + + WPP A C+  
Sbjct 59 CGNTLVITYILRYAKTKTTNIIYLNLAIDLEL-MGLGFLPMQVNLVHMPGKALCRV 117  
Query 119 SGLVQMSVSASVFTLVAIAVERFRCTVHPFREKLTLR--KALVTIAVINALALLMCP 275  
V G+ + S+ F L + + + +R+ +VHP+ R + +T+AV N +LL+ P  
Sbjct 118 VNTGNTQPTISCTVMSIDRYLAVVHPDKSKMRKPRTKAMITWV-MQVSLVLTLP 176  
Query 176 SAVTLTVTREETHHVMDARNRSYPLYSCEWAMPFKGMRRVYTVFLSHI--YLAFLAIV 233  
+ + + + + SC MP + + + + + L PL + +  
Sbjct 177 IMI-----YAGLRSNQWGRSSCTINNPQESGAWGTGYITFTPLGFLVLTIC 225  
Query 234 VMYARIARKLCOAPGAPGGERAADPRASRRRARVHMLVMAFLPFTLSMLPLWALLLI 293  
+ Y I K+ G + + + +V M+ +V P WLP+ + +  
Sbjct 226 LCVLYITIKV-----KSSGIRVGSKKRSEKKVTRMVSIVVAFIPCMPPFY----IF 275

Query 294 DYQQLS----APQLHLVTYAFPFHMLAFFNSSANPIIYGFNFNFRGPOAA-RAR 347  
 +S+ P L + F F L + NS ANP+Y + +NF+ + PQ  
 Sbjct 276 NVSSVSAISPTALKGM----FDVVVLTYSANCAPIYAFGLNFKFSGVCLVK 331

Query 348 LCPSPSGSHKAYSER 363  
 + G +  
 Sbjct 332 VSGTDDGERSDSKQCK 347

>gb|AAH95542.1| **[G]** Neuromedin B receptor [Homo sapiens]  
 Length=390  
 GENE ID: 4829 NMNR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (289), Expect = 2e-25, Method: Compositional matrix adjust.  
 Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)

Query 50 YALIFLCHVGNLTWCFVLNKRHHMTVTNMFILNLAVSDLLGVFCMPTTLVDNLITG 109  
 Y LI + ++GN ++ I + N M +v N+P NLA DIL+ + C+P W  
 Sbjct 50 YLLITITVGLLGNILVKFITNSAMRSVPMFISNLAAAGDLLLLLTCVPVDASRYFFDE 109

Query 110 PPDNATCMGSLVQMGVSASVFTLVAIAVERFCRIVHPFREKLTLRKALVTIAVMA 167  
 F CK + +C SV SVTTLA ++ +R+R TV+P + + L + V W  
 Sbjct 110 MPFGVKCKLIPVILQTSVGVSVFTLTALSADRYRAIVNPMDMQTSALLRCKVAMGIW 169

Query 168 LALLIMCPSAVTLTVTREHHFMDARNRSYPLSCWEAMPEKGM--RVYITVFLSHY 225  
 ++L+ P AV V R + N S+ +C +P+ + + + +F +  
 Sbjct 170 VSVLAVPEAVFSEVAR----ISSLNSSTP--ACT-PYPQDELHPKHSVLPLVYF 221

Query 226 LAPLALIVVMYARIARKLQAPGAPGGEAADPRASRRARVHMLVMVLPFTLSWLP 285  
 L PLR+I + Y IA+ L+ + + PG + R R+ + + + + F M W  
 Sbjct 222 LPLALISIVYCIARKLILASAHNLPGEYNEHTKOMETRGLAKVIVVGVGCFICMP 281

Query 286 LKALLLL--IDYQQLSAPQLHLVTYAFPFHMLAFFNSSANPIIYGFNFNFRGPOAA 343  
 L + +Y ++ H+ + A L+P NS NP +RPR F  
 Sbjct 282 NHILYMRSPHNYNIDPSLGHMIVTLV--ARVLSFGNSCVNPFALYLLSFRHFN-- 336

Query 344 FRALKCPSPSGSHKAYSER 363  
 ++LC ++Y ER  
 Sbjct 337 --SGLC-----CGKSYQER 349

>gb|ABQ52418.1| **[G]** prokineticin receptor 2 [Homo sapiens]  
 Length=384  
 GENE ID: 128674 PROK2 | prokineticin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (289), Expect = 2e-25, Method: Compositional matrix adjust.  
 Identities = 98/373 (26%), Positives = 173/373 (46%), Gaps = 41/373 (10%)

Query 16 SQNGTWTATP-----ATMLTFS-SYVNTSP-----AMFIVAVAL 52  
 +QNG NT TP A++L+P+ SY + P+ AA ++ AL  
 Sbjct 3 AQNG-NTSFTPNFNPQDASHSSIFNFSYGDYLDLDEDEDMTKTRTPFAAKIVIGIALA 61

Query 53 -IFLCHVGNLTWCFVLNKRHHMTVTNMFILNLAVSDLLGVFCMPTTLVDNLITG 109  
 L LC +GN + + + + +TN+ I NLA+SD LV I C P + + + +  
 Sbjct 62 GIMVCGCNLTWCFVLNKRHHMTVTNMFILNLAVSDLLGVFCMPTTLVDNLITG 121

Query 110 PPDNATCMGSLVQMGVSASVFTLVAIAVERFCRIVHPFREKLTLRKALVTIAVMA 169  
 C + +S S L+LH+ + + THD + + A L+M +  
 Sbjct 122 EHGVLCAVNYLRTVSLVSTNLALALAIIDRYLIVHPLCPNNYQASFLIALVMVS 181

Query 170 LLIMCPSAVTLTVTREHHFMDARNRSYPLSCWEAM--EKGMRVYITVFLSHYLA 227  
 +LI PSA T E F+V ++ + + C+MP ++ + Y +F +  
 Sbjct 182 LLIAPISAYFAT--ETVLPVKSQKIP---CQIWPVDQQLYKSYFLPFGVEFVG 234

Query 286 LPLALIVVMYARIARKLQAPGAPGGEAADPRASRRARVHMLVMVLPFTLSWLP 285  
 P + + YAR+ E+L R+ +V M + + A + L H P +  
 Sbjct 235 PVVMTLCYARISRELWKAIVGFGTQIRKRLCRRTVLVIMCILTA--YVLWAFPY 292

Query 288 ALLLLIDYQ-QLSAPQLHLVTYAFPFHMLAFFNSSANPIIYGFNFNFRGPOAA 346  
 ++ D+ + + H+T AP +A NS N + + N + F+  
 Sbjct 293 GFTIVDFPFTVFKKHYLT--AFVVECIAMNSMIMTKCPTVKNNTKVKKMLL 350

Query 347 RLCPRRGCHKRA 359  
 P GQ A  
 Sbjct 351 HWRPSQSGSKSA 363

>ref|NP\_002502.2| **[H]** **[G]** neuromedin B receptor [Homo sapiens]  
 sp|P28336.2|NMNR\_HUMAN **[G]** RecName: Full=Neuromedin-B receptor; Short=NM-B; AltName: Full=Neuromedin-B-preferring bombesin receptor  
 emb|CAK70473.1| **[G]** neuromedin B receptor [Homo sapiens]  
 gb|BAW47886.1| **[G]** neuromedin B receptor [Homo sapiens]  
 Length=390

GENE ID: 4829 NMNR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (288), Expect = 3e-25, Method: Compositional matrix adjust.  
 Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)

Query 50 YALIFLCHVGNLTWCFVLNKRHHMTVTNMFILNLAVSDLLGVFCMPTTLVDNLITG 109  
 Y LI + ++GN ++ I + N M +v N+P NLA DIL+ + C+P W  
 Sbjct 50 YLLITITVGLLGNILVKFITNSAMRSVPMFISNLAAAGDLLLLLTCVPVDASRYFFDE 109

Query 110 PPDNATCMGSLVQMGVSASVFTLVAIAVERFCRIVHPFREKLTLRKALVTIAVMA 167  
 F CK + +C SV SVTTLA ++ +R+R TV+P + + L + V W  
 Sbjct 110 MPFGVKCKLIPVILQTSVGVSVFTLTALSADRYRAIVNPMDMQTSALLRCKVAMGIW 169

Query 168 LALLIMCPSAVTLTVTREHHFMDARNRSYPLSCWEAMPEKGM--RVYITVFLSHY 225  
 ++L+ P AV V R + N S+ +C +P+ + + + +F +  
 Sbjct 170 VSVLAVPEAVFSEVAR----ISSLNSSTP--ACT-PYPQDELHPKHSVLPLVYF 221



Query 226 LAPALIVVMYARIARKLCOAGPAPGGEAAADPRASRRRARVVMHLMVVALFPTLSWLP 285  
 L PLA-I + Y IA+ L ++ PG + R R+ + + + F M P  
 Sbjct 222 LIPLAIIISYYHIAKTLKSAHNLPGYEINHTKQKMETRRLAKIIVLVFGGCFPCWPP 281  
 Query 286 LWALLL--IDYQLSAPQIHLVTVYAPFAHMLAFPNSSANIIYGFNPNFRGQAA 343  
 L + Y + A L P+ NS NP + + PR P  
 Sbjct 282 NHILVMYRSFMYNEIDPSLGHMIVTLV--ARVLSFGNSCVNPFALYLSSESFRHFN-- 336  
 Query 344 FRARLCPRSPSGHKEAYSER 363  
 ++L C ++Y Y ER  
 Sbjct 337 --SGLC-----CGRKSQYER 349

-gb|AAA59939.1| **G** neuromedin B receptor  
 gb|AAB27330.1| **G** neuromedin B receptor, NMB receptor-bombesin-like peptide receptor  
 [human, SCLC cell line H345, Peptide, 390 aa]  
 Length=390

GENE ID: 4829 NMNR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (288), Expect = 3e-25, Method: Compositional matrix adjust.  
 Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)  
 Query 50 YALIFLCVGNLTVCPIVLKRRHMTVMNFIHLAVSDLLWGIFCMPTTLVDNLITW 109  
 Y LI + ++GN ++ I + N M +V N+PI NLA DLL+ C+P W  
 Sbjct 50 YLLIITVGLGNIMLWKIPITNSAMRSVPNIFISNLAAGDLLLTCTVVDASRYFDEW 109  
 Query 110 PFDNATCKMSGLVQMSVSASVFTLVAIAVERFCIVHPFREKLT--LRKALVTIAVIA 167  
 F CK+ +Q SV SVFTL A++ R+R IV+P + + L + V IW  
 Sbjct 110 MFGVCKLPIQLTISVGVSVFTLITLSDRYRAIVNMQMGTSGALLATCTCKMGIW 169  
 Query 168 LALLIMCPASVTLTVTRHEHMFVDARNSYPLYSCEWAEPEKGMK- RYVITVLSHIY 225  
 ++L+ P NV V R H+ N S+ L C +B+ + + + + P  
 Sbjct 170 VSVLVAPEAVFSERAR-----ISLDSST--ACI-PYPOTDELHFKHSVLIFLIVP 221  
 Query 226 LAPALIVVMYARIARKLCOAGPAPGGEAAADPRASRRRARVVMHLMVVALFPTLSWLP 285  
 L PLA-I + Y IA+ L ++ PG + R R+ + + + F M P  
 Sbjct 222 LIPLAIIISYYHIAKTLKSAHNLPGYEINHTKQKMETRRLAKIIVLVFGGCFPCWPP 281  
 Query 286 LWALLL--IDYQLSAPQIHLVTVYAPFAHMLAFPNSSANIIYGFNPNFRGQAA 343  
 L + Y + A L P+ NS NP + + PR P  
 Sbjct 282 NHILVMYRSFMYNEIDPSLGHMIVTLV--ARVLSFGNSCVNPFALYLSSESFRHFN-- 336  
 Query 344 FRARLCPRSPSGHKEAYSER 363  
 ++L C ++Y Y ER  
 Sbjct 337 --SGLC-----CGRKSQYER 349

-gb|AAA36623.1| **G** somatostatin receptor  
 dbj|BAA04106.1| **G** fourth somatostatin receptor subtype [Homo sapiens]  
 gb|AAS55648.1| **G** somatostatin receptor 4 [Homo sapiens]  
 gb|AAN69063.1| **G** Somatostatin receptor 4 [Homo sapiens]  
 gb|AAI17273.1| **G** Somatostatin receptor 4 [Homo sapiens]  
 Length=388

GENE ID: 6754 SSTR4 | somatostatin receptor 4 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (287), Expect = 4e-25, Method: Compositional matrix adjust.  
 Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)  
 Query 50 YALIFLCVGNLTVCPIVLKRRHMTVMNFIHLAVSDLLWGIFCMPTTLVDNLITW 109  
 YAL+ L+ +VGN LV F+L+ M T TN++LNLAV+D L + +P + W  
 Sbjct 54 YALCGLVGNLVLVPIVLVIAKRTATVILLNLAVIDLP+MLSVPPVASSALRHH 112  
 Query 110 PFDNATCKMSGLVQMSVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAV- IKA 167  
 P+ + Y I K+ A+ V+V R+ -VHD P R + + + + W  
 Sbjct 113 PFGSVLCRAVLSDGLNMTFSVFTLTVLSDRYVAVHPLKAATYRRPSVAKLNLGVLW 172  
 Query 168 LALLIMCPASVTLTVTRHEHMFVDAR- NRSYPLYSCEWAEPEKGMRRVITVLSHIY 226  
 ++L+ P A+ D R R +C WP V+ P + L  
 Sbjct 173 ASLVTLPIAI-----PADTRPARGQQAACNLQWHPNAPSAPVVVVTLGLPL 221  
 Query 227 LAPALIVVMYARIARKLCOAGPAPGGEAAADPRASRRRA- RVVIMHLMVVALFPTLSWLP 284  
 P+ T I Y I G + + + R R+ + + + +MY + T L W+  
 Sbjct 222 LPVLAIGLCYLLVGKM-RAVALRAGQQ-----RRSEKKTIRLVLMVVVVLVLCWM 273  
 Query 285 PLWALLL--IDYQLSAPQIHLVTVYAPFAHMLAFPNSSANIIYGFNPNFRGQAA 343  
 P + + LL + L A H+ + L+ NS ANP+YG+ +NPR PQ  
 Sbjct 274 PFYVQLNLLVTSLOATVNHVSLI-----LSYANSCANPLYGLSDNFRSPQV 325  
 Query 344 FRARLC 349  
 R C  
 Sbjct 326 LCLRCC 331

-gb|AAK61266.1|AK006466\_1 **G** somatostatin receptor type 5 [Homo sapiens]  
 Length=364

GENE ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 115 bits (287), Expect = 4e-25, Method: Compositional matrix adjust.  
 Identities = 93/307 (30%), Positives = 146/307 (47%), Gaps = 40/307 (13%)  
 Query 60 GNTLVLCVILGNHMTVMNFIHLAVSDLLWGIFCMPTTLVDNLITWPPDNATCKMS 119  
 GNTLV ++VL+ M TVTN++LNLAV+D L + +P N + WPF C++  
 Sbjct 57 GNTLVIVVLRFAKMTVINYIILNLAVDVLV-MLGLPLATQNAASFPPGVLKRLV 115  
 Query 120 GLVQMSVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTI- AVIALALLIMCPSA 177  
 + G+ SVF L +V R+ +VHP R + + A H L+L + P  
 Sbjct 116 MTLGQVQCFSTVPLCTVNSVDYLAIVHPLSARHRRPRVAKLASAAWVSLCNSLPL 175



(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

Query 50 YALIFLLCMVGNLTVCPIVLKRRHMTVTNMFILNLAUSDLLVGIFCMPTTLVDNLITGW 109  
YAL+ L+ +VGN LV F+L+ M T TN++LNLAV+D L + +P + + W  
Sbjct 54 YALVCLVGLGNALVIFVILRYAKMTATNIYLLNLAVADELF-MLSVPFVASSAALRHW 112  
Query 110 PFDNATCKMSGLVQMSVSASVPTLVAIAVERFCRIVHPFREKILTRKALATIAV--IWA 167  
PF + C+ V G++ SVF L ++V+R+ +VHP R R++ + +M  
Sbjct 113 PFGSVLCRAVLSVGLNMTFVCLTVLSVDVRYAVVHPLRAATYRRSPVAKLNLGVWL 172  
Query 168 LALLIMCPASVLTITVREEHFMVDAR-NRSYPLYSCEWAMPEKMRVVTYVLFHSIYL 226  
+LL+ P A+ D R R + +C WP V+ F + L  
Sbjct 173 ASLVLTLPIAI-----FADTSPARGQQAACNLQWHPANSAVVFVYTLGLFL 221  
Query 227 APALIVVMYARIARLKLCPGAPAGGEEADPRASRRA--RVVHMLVMVLFPTLSLW 284  
P+ I + Y I K+ +A G ++ RER+ ++ ++MV + F L W+  
Sbjct 222 LPVLAIQLCYLLIVGRN-RAVALRAGWQO-----RRSEKILTRVLMVVFVFLCWM 273  
Query 285 PLWALLLL-IDYQLSAPOLHLVTYVAFPAHWAFFNNSANPIIYGYPNFRFGQAA 343  
P + + LL + L A H+ + L++ NS ANPI+YG+ +NFR FQ  
Sbjct 274 PFTYVGLNLFLVTSLDATVHVSLLI-----LSYANSCANPIYGLSDNFRFPFRQV 325  
Query 344 FRALRC 349  
R C  
Sbjct 326 LCLRC 331

>gb|AA87342.1| **G** DRG kappa 1 splice variant KOR 1A [Homo sapiens]  
Length=366

GENE ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 97/340 (28%), Positives = 164/340 (48%), Gaps = 40/340 (11%)

Query 8 PNNSWPLSQNGTNTATPATNLTFSSYQHTSPVAMFIVA-YALIFLLCMVGNLTVCPI 66  
PNNS + + PA H SD + I A Y++P++ +VGR+LV F  
Sbjct 23 PNNS---AGSEDAQLPA-----HISPAIVITVYAVVAVVGLVGLSVLP 68  
Query 67 IVLNRRHMTVTNMFILNLAUSDLLVGIFCMPTTLVDNLITGWPFNATCKMSGLVQMS 126  
++M C T TH++I HLA++D LV MP L+ MPP +A CK+  
Sbjct 69 VIIRYTKMTATNIYIFNLALADALVTT-TMPFQSTVYLMNSKPFQDALCKIVISIDYN 127  
Query 127 VSASVPTLVAIAVERFCRIVHPFREKILTR--KALVTIAVIMALLIMCPASVLTITV 183  
+ S+PTL ++V+R+ + HP + L R KA + IM L+ + SA+ L T  
Sbjct 128 MFTSIFLTMTMSVDRIYAVCHPVK-ALDFRTPLKAKIINICWLLSSGVI-SAILVGGT 185  
Query 184 REEHFMVDARNKSY-LSYCEWAMPEKMRVVTYVLFHSIYLAPALIVVMYARIAR 241  
+ V + +P TS W+ + +F ++ P+ +I+V Y +  
Sbjct 186 KVREDVDVIECSLQFPDDDYSHWDLFMK-----ICVIFAFVPLVILIIYCVTLML 237  
Query 242 KLCPGAPAGGEEADPRASRRA--RVVHMLVMVLFPTLSLWPLWALLIDYQLSAP 301  
+L++ G E R R R+ ++V F + W P+ +L+ G S  
Sbjct 238 LR-KSVRLSGSRE----KDRNLRIITRLVLVVAVVFCVCPHIHIFILVGLGSTSHS 291  
Query 302 QLHLVTYVAFPAHWAFFNNSANPIIYGYPNFRFGQAA 341  
L + Y F L + NSS NDI+Y + +RNF R F+  
Sbjct 292 TAAISSTY----PCIALGTNSSLNFIYAPLDFNFRFCR 328

>gb|BX10169.1| **G** somatostatin receptor 4, isoform CRA\_b [Homo sapiens]  
Length=389

GENE ID: 6754 STR4 | somatostatin receptor 4 [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

Query 50 YALIFLLCMVGNLTVCPIVLKRRHMTVTNMFILNLAUSDLLVGIFCMPTTLVDNLITGW 109  
YAL+ L+ +VGN LV F+L+ M T TN++LNLAV+D L + +P + + W  
Sbjct 54 YALVCLVGLGNALVIFVILRYAKMTATNIYLLNLAVADELF-MLSVPFVASSAALRHW 112  
Query 110 PFDNATCKMSGLVQMSVSASVPTLVAIAVERFCRIVHPFREKILTRKALATIAV--IWA 167  
PF + C+ V G++ SVF L ++V+R+ +VHP R R++ + +M  
Sbjct 113 PFGSVLCRAVLSVGLNMTFVCLTVLSVDVRYAVVHPLRAATYRRSPVAKLNLGVWL 172  
Query 168 LALLIMCPASVLTITVREEHFMVDAR-NRSYPLYSCEWAMPEKMRVVTYVLFHSIYL 226  
+LL+ P A+ D R R + +C WP V+ F + L  
Sbjct 173 ASLVLTLPIAI-----FADTSPARGQQAACNLQWHPANSAVVFVYTLGLFL 221  
Query 227 APALIVVMYARIARLKLCPGAPAGGEEADPRASRRA--RVVHMLVMVLFPTLSLW 284  
P+ I + Y I K+ +A G ++ RER+ ++ ++MV + F L W+  
Sbjct 222 LPVLAIQLCYLLIVGRN-RAVALRAGWQO-----RRSEKILTRVLMVVFVFLCWM 273  
Query 285 PLWALLLL-IDYQLSAPOLHLVTYVAFPAHWAFFNNSANPIIYGYPNFRFGQAA 343  
P + + LL + L A H+ + L++ NS ANPI+YG+ +NFR FQ  
Sbjct 274 PFTYVGLNLFLVTSLDATVHVSLLI-----LSYANSCANPIYGLSDNFRFPFRQV 325  
Query 344 FRALRC 349  
R C  
Sbjct 326 LCLRC 331

>emb|CAH73066.1| **G** prolactin releasing hormone receptor [Homo sapiens]  
Length=370

GENE ID: 2834 PRHR | prolactin releasing hormone receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 99/305 (32%), Positives = 152/305 (49%), Gaps = 25/305 (8%)

Query 60 GHTLVCPVLNRRHMTVTNMFILNLAUSDLLVGIFCMPTTLVDNLITGWPFNATCKM 118

Sbjct 77 GN L- ++ R +H VTN I NLA+SD+L- C+P TL GW P C + 136  
GNCLLVIAIRVRRLNVTNVLGNLSDVLMCTACVPLTAYAFEPGRHVGGLCHL

Query 119 SGLVQMSVSAVPTTVAIAVERFRICVHPFREKLTLRKALVTIAVIMALLIMCPAV 178  
++ V+ SVPTL TAY+R+ +VHP R ++LR + + IHAL+ ++ P+AV

Sbjct 137 VFLLQPTVTVYVSPTLTITIAVDRTVVLVPLRRIRISRLSAYAVLAIWASVLAALPAV 196  
VFLLQPTVTVYVSPTLTITIAVDRTVVLVPLRRIRISRLSAYAVLAIWASVLAALPAV

Query 179 TLTVTREHHFMDARNRSPLYSCHEAM-PEKGMRRVTTVLFPSHIYLAFLALVIMYA 237  
H + V+ + C E W ++ R+Y L YL PL I++ Y

Sbjct 197 -----HTYVVLKPDVRL-CEPFMSQERQRYAGMLLVTVLLVLAVILSYV 246  
-----HTYVVLKPDVRL-CEPFMSQERQRYAGMLLVTVLLVLAVILSYV

Query 238 RIARKLQCAQPAQGEAEADPRASRRARVVMHVMVALFPTLSMLMLWALLLLIDYQG 297  
R+ KL P+ AD +RR +LV++ + F +WHL LL D

Sbjct 247 RVSVKLNRNVRPGCVTSQADMDRARRRRTFC-LLVVIVVFAVCNLEPLVFNLLRLDLP 305  
RVSVKLNRNVRPGCVTSQADMDRARRRRTFC-LLVVIVVFAVCNLEPLVFNLLRLDLP

Query 298 LSAQPLHLVTVYAF----FAHNLAFPNSSAMPIIYGPNFRFGQAFARLRCPRS 353  
H + YAF HWLA ++ NP IY + ++PR + A PR

Sbjct 306 -----HAIDPIAFGLVQLLCHWLMSSACINPFIYAWLHDSFRELKLLVAM--PRKI 357  
-----HAIDPIAFGLVQLLCHWLMSSACINPFIYAWLHDSFRELKLLVAM--PRKI

Query 354 GSHKE 358  
H +

Sbjct 358 APHQ 362

>dbj|BAF82684.1| [C] unnamed protein product [Homo sapiens]  
Length=384

GENE ID: 128674 PROKR2 | prokineticin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 97/373 (26%), Positives = 172/373 (46%), Gaps = 41/373 (10%)

Query 16 SONGNTTATP-----ATNLTFPS-SYQVOTSP-----AAMFIVAYAL- 52  
+QNG NT TP A++L+P+ SY + D+ AA ++ AL

Sbjct 3 AQNG-NTSPTFNFPQDQASSLSFNFSYGDYLDMDDEDMTKTRTPFAKIVIGIALA 61  
AQNG-NTSPTFNFPQDQASSLSFNFSYGDYLDMDDEDMTKTRTPFAKIVIGIALA

Query 53 -ITFLCMVGNLTVCFTVLKNNHMTVTNMFILNLAVSDLLWGIFCPMPTLVNLTG- 109  
I L C + GN + + + + -TH+ I NLA+SD LV I C P + ++ W

Sbjct 62 GTMLVCGISGNFVIALYTKLEHLNLTLLIANLAISDFLVAICCPFEDMYVQVGLSW 121  
GTMLVCGISGNFVIALYTKLEHLNLTLLIANLAISDFLVAICCPFEDMYVQVGLSW

Query 110 FPDNATCMQSGLVQMSVSAVPTTVAIAVERFRICVHPFREKLTLRKALVTIAVIMALA 169  
+ C ++ +S S L+ATA+R+ IVHP + ++ A I++W ++

Sbjct 122 EHGHLVCSAVNYLTVSLVYSTNALLATAIDRYALTIVPLKPRMNTQASFLIALVMVMS 181  
EHGHLVCSAVNYLTVSLVYSTNALLATAIDRYALTIVPLKPRMNTQASFLIALVMVMS

Query 170 LLIMCPASAVLTVTREHHFMDARNRSPLYSCHEAM-PEKGMRRVTTVLFPSHIYLA 227  
+LI PSA T T E P+V++ + C + WP ++ + Y + P ++

Sbjct 182 LLIMCPASAVT--FTVLFIVSGRITP---CQIMFVQDLVYKSYFLFPGVETFG 234  
LLIMCPASAVT--FTVLFIVSGRITP---CQIMFVQDLVYKSYFLFPGVETFG

Query 228 PLALVIMVYARIARLQCAQPAQGEAEADPRASRRARVVMHVMVALFPTLSMLPLW 287  
P L + + YARI+R+L P E+ RR+ +V M ++ A + L W P +

Sbjct 235 PVVNTILCYARISRELWFKAVPGFQTDQIRKRLCCRKTVLVLMCLTA--YVLCWAPY 292  
PVVNTILCYARISRELWFKAVPGFQTDQIRKRLCCRKTVLVLMCLTA--YVLCWAPY

Query 288 ALLLLIDYG-QLSAQPLHLVTVYAFPAHNLAFPNSSAMPIIYGPNFRFGQAFRA 346  
++ D+ + + H +T AF +A NS + + N + P+ +

Sbjct 293 GFTIVRDFPFPVVKKEVILT--APYVVECIAMSSIMVTVCPTVKNMTKPKKEMML 350  
GFTIVRDFPFPVVKKEVILT--APYVVECIAMSSIMVTVCPTVKNMTKPKKEMML

Query 347 RLCPRSGSHKEA 359  
P C A A

Sbjct 351 HWRPSQSGKSSA 363  
HWRPSQSGKSSA 363

>gb|AAA6565.1| [C] somatostatin receptor  
Length=388

GENE ID: 6754 SSTPR4 | somatostatin receptor 4 [Homo sapiens]  
(Over 10 PubMed links)

Score = 112 bits (280), Expect = 2e-24, Method: Compositional matrix adjust.  
Identities = 91/306 (29%), Positives = 149/306 (48%), Gaps = 34/306 (11%)

Query 50 YALIFLLCMVGNLTVCFTVLKNNHMTVTNMFILNLAVSDLLWGIFCPMPTLVNLTG- 109  
YAL+ L+ +VGN LV F++L+ M T T ++LNLAVD L + +P + W

Sbjct 54 YALVCLVGLVGNALVIFVILRVARAKTATTIYLLNLAVADLFP-MLSVFPVASSAALRH 112  
YALVCLVGLVGNALVIFVILRVARAKTATTIYLLNLAVADLFP-MLSVFPVASSAALRH

Query 110 FPDNATCMQSGLVQMSVSAVPTTVAIAVERFRICVHPFREKLTLRKALVTIA--VHA 167  
P+ T + Y I G+ + SVF L + +V+R+ +VHP R + + + W

Sbjct 113 PFGSVLCRAVLSDVGLNMTFSPCLTIVLSDVRYAVVHPLRAATYRRPVAKLINVLNL 172  
PFGSVLCRAVLSDVGLNMTFSPCLTIVLSDVRYAVVHPLRAATYRRPVAKLINVLNL

Query 168 LALLIMCPASAVLTVTREHHFMDARNRSPLYSCHEAM-PEKGMRRVTTVLFPSHIYLA 226  
+LL+ P+ + D R R + C + WP V+ F +L

Sbjct 173 +LLVTLFIALI-----PADTRPAGGQAVACHLQWHPMSAVFVVVTLGLGL 221  
+LLVTLFIALI-----PADTRPAGGQAVACHLQWHPMSAVFVVVTLGLGL

Query 227 APLALVIMVYARIARLQCAQPAQGEAEADPRASRRARVVMHVMVALFPTLSML 284  
P+ T + Y I G+ + SVF L + +V+R+ +VHP R + + + W

Sbjct 222 LFLVALGLCYLLVIGDM-RAVALRAGWQ-----RRSEKKTILVLMVVVFLVCM 273  
LFLVALGLCYLLVIGDM-RAVALRAGWQ-----RRSEKKTILVLMVVVFLVCM

Query 285 PLWALLLL-IDYQGLSAQPLHLVTVYAFPAHNLAFPNSSAMPIIYGPNFRFGQAFRA 343  
P + + LL + L A H+ + L+ NS ANFI+YG+ ++NPR PQ

Sbjct 274 PFFVQVLNLNVTSIDATVNHVSLI-----LSYANSCANILYGLSDNPRSPQRV 325  
PFFVQVLNLNVTSIDATVNHVSLI-----LSYANSCANILYGLSDNPRSPQRV

Query 344 FRALRC 349  
R C

Sbjct 326 LCLRC 331  
LCLRC 331

>dbj|BAJ6542.1| [C] unnamed protein product [Homo sapiens]  
Length=164

GENE ID: 4866 NPY1R | neuropeptide Y receptor Y1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 110 bits (276), Expect = 6e-24, Method: Compositional matrix adjust.  
Identities = 68/171 (39%), Positives = 96/171 (56%), Gaps = 5/171 (2%)

Query 74 MHTVTNMFILNLAVSDLLWGIFCPMPTLVNLTGWPFDNATCMQSGLVQMSVSAVPT 133  
M VTN+ I+RL+ SDLLV I C+P T V L+ W F A CK+ + VQ +S+ +S+P+

Sbjct 1 MRNVNITILVNLSPSDDLVAIMCLPPTFVYTLMDRWVGEAMCKINFPVQCVSITVSIFS 60  
MRNVNITILVNLSPSDDLVAIMCLPPTFVYTLMDRWVGEAMCKINFPVQCVSITVSIFS

Query 134 LVAIAVERFCRIVHPFKRLTLKALVTIAVIALALLMCPASVTLTVTRE-EHHFMD 192  
 LV IAYER + I + F + + R A V IAVIN LA + P + T E + + D  
 Sbjct 61 LVLIAVERFCRLINFGGWRPNRRAVGLAVIWLVAVASSLPFLIYQWTRDFPQWTLTD 120

Query 193 ARNSYPLYSCHWAMPEKGRMRYVTVLFSHIYLAFLALIVMYARIARL 243  
 A Y C + Y + + EL I Y + + R  
 Sbjct 121 AYKDK---YVCFDQPSDSHRLSYTLLLLVLQYFGPLCFICYFKV-RKL 167

>gb|AA021070.1|AF498922\_1 [G] opioid receptor kappa [Homo sapiens]

gb|AA020985.1| [G] kappa opioid receptor

dbj|BA035888.1| [G] unnamed protein product [Homo sapiens]  
 Length=380

GENE ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (276), Expect = 6e-24, Method: Compositional matrix adjust.  
 Identities = 89/310 (28%), Positives = 154/310 (49%), Gaps = 26/310 (8%)

Query 38 HTSPVAAMFIVA-YALIFLLCWGNLTVCFVLKRNHMTVTNMFILNLAUSDLLVGIFC 96  
 H SP + I A Y+++F++ +VGN+LV F+++ M T TN++I NLA++D LV  
 Sbjct 53 HISPAIVITAVTSVVFVVLGNSLVNMFVIRITKMTATNIIYFNALADALAVTT-T 111

Query 97 MPTLVNLTITGHPFNATCKMSGLVQMSVSASVFTLVAIAVERFCRIVHPFKRLTLR 156  
 MP L+ MFP + C+ + S+PTL ++V R+ + HP + L R  
 Sbjct 112 MPQSTVYLMNSMPFDVLCIKVISIDYYNMFISITFLTNMSVRYIAVCHPVK-ALDFR 170

Query 157 ---KALVTIAVIALALLMCPASVTLTVTREHHFMDARNRSYP--LYSCHEWPEKG 211  
 KA + IW L+ + SA+ L T+ V + + P YS++ + +  
 Sbjct 171 TPLKAKIINICWLLSSVGI-SAILVIGTKVREDVDVIECSLQFPDDOYNSWDLFMK-- 227

Query 212 MRRVYTVLFSHIYLAFLALIVMYARIARLCAQPGAPGKEEADPRASRRRVRVHM 271  
 +F ++ P+ +I V Y + +L ++ G E R R+ +  
 Sbjct 238 -----ICVFIFAFVPIVLIIVCTYTLMLRL-KSVRLSSGRE----KDRNLARITRL 275

Query 272 LVMVLFPTLSKLPWALLLLIDYQLSAPQLHLVTUVYAFFFAHNLWLAFFNNSANPIIYGY 331  
 ++V F + W P+ +L+ G S L + Y F L + NS NPI+Y +  
 Sbjct 276 VLVVVAVFVVCMTPIHIFILVEALGSTSHSTAALSSY---FCIALGYTNSLNPILYAF 332

Query 332 FNFNFRFGFC 341  
 +ENF+R F+  
 Sbjct 333 LDENFKRCFR 342

>ref|NP\_000903.2| [G] opioid receptor, kappa 1 [Homo sapiens]

sp|P41145.2|OPRK1 HUMAN [G] RecName: Full=Kappa-type opioid receptor; AltName: Full=KOR-1

gb|AAC50158.1| [G] kappa opioid receptor

gb|AAA63906.1| [G] kappa opioid receptor

gb|AAH9912.1| [G] Opioid receptor, kappa 1 [Homo sapiens]

gb|BAW86723.1| [G] opioid receptor, kappa 1 [Homo sapiens]

prf|2104381A kappa opioid receptor

Length=380

GENE ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (276), Expect = 7e-24, Method: Compositional matrix adjust.  
 Identities = 89/310 (28%), Positives = 154/310 (49%), Gaps = 26/310 (8%)

Query 38 HTSPVAAMFIVA-YALIFLLCWGNLTVCFVLKRNHMTVTNMFILNLAUSDLLVGIFC 96  
 H SP + I A Y+++F++ +VGN+LV F+++ M T TN++I NLA++D LV  
 Sbjct 53 HISPAIVITAVTSVVFVVLGNSLVNMFVIRITKMTATNIIYFNALADALAVTT-T 111

Query 97 MPTLVNLTITGHPFNATCKMSGLVQMSVSASVFTLVAIAVERFCRIVHPFKRLTLR 156  
 MP L+ MFP + C+ + S+PTL ++V R+ + HP + L R  
 Sbjct 112 MPQSTVYLMNSMPFDVLCIKVISIDYYNMFISITFLTNMSVRYIAVCHPVK-ALDFR 170

Query 157 ---KALVTIAVIALALLMCPASVTLTVTREHHFMDARNRSYP--LYSCHEWPEKG 211  
 KA + IW L+ + SA+ L T+ V + + P YS++ + +  
 Sbjct 171 TPLKAKIINICWLLSSVGI-SAILVIGTKVREDVDVIECSLQFPDDOYNSWDLFMK-- 227

Query 212 MRRVYTVLFSHIYLAFLALIVMYARIARLCAQPGAPGKEEADPRASRRRVRVHM 271  
 +F ++ P+ +I V Y + +L ++ G E R R+ +  
 Sbjct 228 -----ICVFIFAFVPIVLIIVCTYTLMLRL-KSVRLSSGRE----KDRNLARITRL 275

Query 272 LVMVLFPTLSKLPWALLLLIDYQLSAPQLHLVTUVYAFFFAHNLWLAFFNNSANPIIYGY 331  
 ++V F + W P+ +L+ G S L + Y F L + NS NPI+Y +  
 Sbjct 276 VLVVVAVFVVCMTPIHIFILVEALGSTSHSTAALSSY---FCIALGYTNSLNPILYAF 332

Query 332 FNFNFRFGFC 341  
 +ENF+R F+  
 Sbjct 333 LDENFKRCFR 342

>gb|AA032829.1|AF441129\_1 [G] cholecystokinin-C receptor [Homo sapiens]

gb|AAK38351.1| [G] CCK-B/gastrin receptor variant [Homo sapiens]

Length=516

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (276), Expect = 8e-24, Method: Compositional matrix adjust.  
 Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

Query 44 AMPIYAYALIFLLCWGNLTVCFVLKRNHMTVTNMFILNLAUSDLLVGIFCMTPLVD 103  
 A I Ya+IFL+ GH L+ + +R + FTVN F+L+LAVSLD+ + CHP TL+  
 Sbjct 55 ARITVAVITLPMVSGVGMNIIIVLGLSRRTVYAFALFSLVSDLLVAACHNFTLP 114

Query 104 NLITQHPFNATCKMSGLVQMSVSASVFTLVAIAVERFCRIVHPFKRL--TLKALVT 161  
 NL+ + F CK + G+SVS S +LVAI+ER+ I P+ + T A

Sbjct 115 NLWGTFPIPTGVICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARV 174  
 Query 162 IAVWALLALLIMCPSAVTLVTREBHFMVDARNRSYPLYSCHNEAWPEKMRVYTVTLF 221  
 I W L+ L+M P V V C W P +R+ ++ L  
 Sbjct 175 IVATNLLSGLLMVPPYVTVTVQVPGPRVL-----QCVRHWPASRVQRTMSVLL 223  
 Query 222 SHIYLAPLALIVMYARIARKL 243  
 ++ P ++ V Y I+R+L  
 Sbjct 224 LLLFFIPGVVMVAYGLISREL 245

Score = 43.9 bits (102), Expect = 0.001, Method: Compositional matrix adjust.  
 Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 ACPGAPGGEAADPRASRRRARVHMLVWALFPTLSLWPLWALLLLIDYQGLSAPQILH 305  
 ACPG G +++R VV ML+++ + P L WLP+++ + P H  
 Sbjct 380 ACPGSGSGSRPTQAKLLAKKR--VVRMLLIVVLFFLCMLPVYS--ANTWRAPDGPQAH 434

Query 306 VTVYA-PPFAHMLAFPNSANPIIYGPNFNER 338  
 A P H L++ ++ NP+Y + + PR+  
 Sbjct 435 ALSGAPISFIHLLSYASACVPLVYCFMRRFRQ 468

>gb|EAW68734.1| **G** cholecystokinin B receptor, isoform CRA\_a [Homo sapiens]  
 Length=516

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 110 bits (275), Expect = 1e-23, Method: Compositional matrix adjust.  
 Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

Query 44 AMFIVAYAILFLACVGNITVCFIVLNRHMHVITWMLFNLNLSVLDLWGPCMPTTVD 103  
 A+ I Y+ILFL+ GN L+ ++ +R+ TVTN F+L+L+SDLL+ + CMP T+L  
 Sbjct 55 AIRITLAVIPLMSVGNMLITVIGLSRRLRTVTNAPLLSLVSDLLAVACMPPTLLP 114

Query 104 NLITGHPDNATCKMSGLVQMSVASVFTLVAIAVERPRCIVHPFREKL--TLRKALVT 161  
 NL+ + F CK + G+SVS S +LVAIA+ER+ I P + ++ T A  
 Sbjct 115 NLWGTFPIPTGVICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARV 174

Query 162 IAVWALLALLIMCPSAVTLVTREBHFMVDARNRSYPLYSCHNEAWPEKMRVYTVTLF 221  
 I W L+ L+M P V V C W P +R+ ++ L  
 Sbjct 175 IVATNLLSGLLMVPPYVTVTVQVPGPRVL-----QCVRHWPASRVQRTMSVLL 223

Query 222 SHIYLAPLALIVMYARIARKL 243  
 ++ P ++ V Y I+R+L  
 Sbjct 224 LLLFFIPGVVMVAYGLISREL 245

Score = 43.9 bits (102), Expect = 0.001, Method: Compositional matrix adjust.  
 Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 ACPGAPGGEAADPRASRRRARVHMLVWALFPTLSLWPLWALLLLIDYQGLSAPQILH 305  
 ACPG G +++R VV ML+++ + P L WLP+++ + P H  
 Sbjct 380 ACPGSGSGSRPTQAKLLAKKR--VVRMLLIVVLFFLCMLPVYS--ANTWRAPDGPQAH 434

Query 306 VTVYA-PPFAHMLAFPNSANPIIYGPNFNER 338  
 A P H L++ ++ NP+Y + + PR+  
 Sbjct 435 ALSGAPISFIHLLSYASACVPLVYCFMRRFRQ 468

>gb|EAX05261.1| **G** G protein-coupled receptor 103, isoform CRA\_a [Homo sapiens]  
 Length=258

GENE ID: 84193 GPRFR | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 110 bits (274), Expect = 1e-23, Method: Compositional matrix adjust.  
 Identities = 62/181 (34%), Positives = 101/181 (55%), Gaps = 8/181 (4%)

Query 51 ALIFLLACVGNITLVCPIVLNRHMHVITWMLFNLNLSVLDLWGPCMPTTVDLITWMP 110  
 LIF L+ GN LV +V +++ M TVTN+FI +L+L+SDLL+ PC+P T++ N+ W  
 Sbjct 53 VLIFLALAGNALVFPYVTVTKSMKARTVNTIFCSIALSDLLITFCIPVTMLQNTSDMWL 112

Query 111 FDNATCKMSGLVQMSVASVFTLVAIAVERPRCIVHPFREK--TLRKALVTIAYWAL 168  
 CNM VQ +V + T+ IAVER+ +VHP+ K T R+R+ +V+M+ +  
 Sbjct 113 GAGFICGLVQVQSGTAVTEILTNCTIAVERIQGLVHPFMKQVNTSGAFTMLGVVLV 172

Query 169 ALLIMCPSAVTLVTREBHFMVDARNRSYPLYSCHNEAWPEKMRVYTVTLFVSHIYLAP 228  
 A+++ P + + ++ P+ + C E W +++YTT + ++L P  
 Sbjct 173 AVIGSGPMH-HVQGLEIKYDPLYKEH-----ICCLEWTSVPVQKIVITTTFILVLFLP 226

Query 229 L 229  
 L  
 Sbjct 227 L 227

>ref|NP\_795344.1| **G** cholecystokinin B receptor [Homo sapiens]  
 sp|P32239.1|GASR\_HUMAN **G** RecName: Full=Gastrin/cholecystokinin type B receptor; Short=CCK-B  
 receptor; Short=CCK-BR; AltName: Full=Cholecystokinin-2  
 receptor; Short=CCK2-R  
 gb|AAA35660.1| **G** cholecystokinin receptor  
 10 more sequence titles

gb|AAA35657.1| **G** cholecystokinin-B/gastrin receptor  
 gb|AAC37528.1| **G** gastrin receptor  
 dbj|BAA02564.1| **G** cholecystokinin receptor [Homo sapiens]  
 gb|AAH00740.1| **G** cholecystokinin B receptor [Homo sapiens]  
 dbj|BAA04759.2| **G** cholecystokinin-B receptor/gastrin receptor [Homo sapiens]  
 gb|AAP35435.1| **G** cholecystokinin B receptor [Homo sapiens]  
 gb|AAP84364.1| **G** cholecystokinin B receptor [Homo sapiens]  
 Length=447

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 110 bits (274), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

Query 44 AMFIVAYALIFLLCMVNTLVCFIVLKNHMHVTVMPTILNLAVSDLLVGFICMPTPLVD 103  
A + I Y A I F L + + G N L + + + R + T V N F L L A V S D L L + C M P T L +  
Sbjct 55 AIRITIVAVIFLAVSGVGMILIVLGLSRLRTVTNMFILNLAVSDLLVAVACMPTPLP 114

Query 104 NLITGWFPDNATCMSGLVQMSVGSASVFTLVAVIAVERFRIVHPFREKL -TLRKALVT 161  
N L + + F C K + G + S V S + L V A I A + E R + I P + + T A  
Sbjct 115 NLMGTFIPGTVICAVSYLGVSVSTLSLVAIALERYSACRPLQARVQTRSHAARV 174

Query 162 IAVIALALLIMCPSAVTLTVTREHHFMVDARNRSPYLSYSCWAEKMGHRVYTVTVLF 221  
I W L + L M P V V + C W P + R + + + L  
Sbjct 175 IVATWLSGLLWVPYVTVTVQVQVGRVL - - - - - CQVHRMPSARVQVTSVLL 223

Query 222 SHIVLPLALIVVMYARIARL 243  
+ P + V Y I R + L  
Sbjct 224 LLLFFIPGVVMVAVAGLSIREL 245

Score = 44.3 bits (103), Expect = 7e-04, Method: Compositional matrix adjust.  
Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 ACPGAPGGEBAADPRASRRRNVHMLVVALFPTLSNLPMLALLIDYQGLSAPOLHL 305  
A P G P G + + + + R V V M L + + + F L W L P + + + P H  
Sbjct 311 ACPGSGSRPTQAKLAKR - - - - - VVRMLVTVLFLCNLFVYS - - - - - ANTWRAFDPGARH 365

Query 306 VTVYA-PPFAHMLAFNNSANIIYGVNFNFR 338  
A F H L + + + N P + Y + + F R +  
Sbjct 366 ALSGAPISPHILSYASACVNPVLVYCPMHRFRQ 399

>gb|AAB30766.2| [C] cholecystokinin B receptor [Homo sapiens]  
Length=447

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 109 bits (273), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

Query 44 AMFIVAYALIFLLCMVNTLVCFIVLKNHMHVTVMPTILNLAVSDLLVGFICMPTPLVD 103  
A + I Y A I F L + + G N L + + + R + T V N F L L A V S D L L + C M P T L +  
Sbjct 55 AIRITIVAVIFLAVSGVGMILIVLGLSRLRTVTNMFILNLAVSDLLVAVACMPTPLP 114

Query 104 NLITGWFPDNATCMSGLVQMSVGSASVFTLVAVIAVERFRIVHPFREKL -TLRKALVT 161  
N L + + F C K + G + S V S + L V A I A + E R + I P + + T A  
Sbjct 115 NLMGTFIPGTVICAVSYLGVSVSTLSLVAIALERYSACRPLQARVQTRSHAARV 174

Query 162 IAVIALALLIMCPSAVTLTVTREHHFMVDARNRSPYLSYSCWAEKMGHRVYTVTVLF 221  
I W L + L M P V V + C W P + R + + + L  
Sbjct 175 IVATWLSGLLWVPYVTVTVQVQVGRVL - - - - - CQVHRMPSARVQVTSVLL 223

Query 222 SHIVLPLALIVVMYARIARL 243  
+ P + V Y I R + L  
Sbjct 224 LLLFFIPGVVMVAVAGLSIREL 245

Score = 44.7 bits (104), Expect = 7e-04, Method: Compositional matrix adjust.  
Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 ACPGAPGGEBAADPRASRRRNVHMLVVALFPTLSNLPMLALLIDYQGLSAPOLHL 305  
A P G P G + + + + R V V M L + + + F L W L P + + + P H  
Sbjct 311 ACPGSGSRPTQAKLAKR - - - - - VVRMLVTVLFLCNLFVYS - - - - - ANTWRAFDPGARH 365

Query 306 VTVYA-PPFAHMLAFNNSANIIYGVNFNFR 338  
A F H L + + + N P + Y + + F R +  
Sbjct 366 ALSGAPISPHILSYASACVNPVLVYCPMHRFRQ 399

>ref|NP\_001040.1| [C] somatostatin receptor 1 [Homo sapiens]  
[P30872.1] [SRI] HUMAN [C] RecName: Full=Somatostatin receptor type 1; AltName: Full=SSR1;  
AltName: Full=SRIF-2  
9 more sequence titles

gb|AA58247.1| [C] somatostatin receptor isoform 1  
gb|AAB35618.1| [C] Somatostatin receptor 1 [Homo sapiens]  
gb|AAP84349.1| [C] somatostatin receptor 1 [Homo sapiens]  
gb|EAW65836.1| [C] somatostatin receptor 1 [Homo sapiens]  
Length=391

GENE ID: 6751 SSTRL1 | somatostatin receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 109 bits (273), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 87/330 (26%), Positives = 160/330 (48%), Gaps = 44/330 (13%)

Query 16 SQNGNTTEATPNLTSSYQHTSPVAMFIVAYALIFLLCMVNTLVCFIVLKNHMH 75  
SQNGT + R S + F I Y + + L + G N + V + + L M  
Sbjct 46 SQNGTSLSDG - - - - - OGSAILISFI - - - - - YSVVCLVGLGNSMIVTVILYARMK 90

Query 96 VTNMFILNLAVSDLLVGFICMPTPLVDNLITGWFPDNATCMSGLVQMSVGSASVFTLV 135  
T T H + I L N L + D L + + P + L + P N P  
Sbjct 91 TATNIIYINLAIDELL - MLSVPPFLVITSLLRHWPFGALLCRLVLSVDVANNMPTSIYCLT 149

Query 136 AJAVERFRIVHPFREKLTLRKALVTIAV - IVALALLIMCPSAVTLTVTREHHFMVDA 193  
+ + V + R + + V R P + R + + + W L L L + P V + F A  
Sbjct 150 VLSVDYVAVVVRPIKAARYRRTPAKVNLGVVWVLSLVLPIVV - - - - - FSRTA 199

Query 194 RNRSPYLSYSCWAEKMGHRVYTVTVLFSHI - VLAPLALIVVMYARIARLQAPGAP 251  
N S + C P E R + V L + + + L P + I + Y I R +

Sbjct 200 AN SDGTVACNMIMPEPAQRNLVGFVLYTFLMGFLLPVGAICLCYVLIIAKRMHV----- 253  
 Query 252 GGEAANDPRARRRRRVVHMLVVALFFTLSHLPLMALLLLDYQQLSAPQLHLVTVYAF 311  
 Sbjct 254 -ALKAGWQQRKRSEKITLHVMVMVVMVFMCHMPFTVVLQVNVFAEQDDATVSQLSVI-- 310  
 Query 312 PFAHMLAFPNSANPIIVGYFMENFRGPO 341  
 L + NS ANFI+YG+ +NP+R PQ  
 Sbjct 311 -----LGYANSCANPILYGFLSDNPKRSQ 335

>gb|EAW68735.1| **C** cholecystokinin B receptor, isoform CRA\_b [Homo sapiens]  
 Length=447

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 109 bits (273), Expect = 2e-23, Method: Compositional matrix adjust.  
 Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

Query 44 AMFIVAVALIFLLCHVNTLVCFIVLQNRHMHVTVNMFIHLNLAUSDLLVGIFCMPTTLVD 103  
 A+ I YA+FL+ +GN L+ + +R+ TVTM F+L+LAUSDLL+ +CH+ FL+  
 Sbjct 55 AIRITLAVAVIFLMSVGGNMLITVVLGLSERLRTVTVNAFLSLAVSDLLAVACMPFTLLP 114  
 Query 104 NLITGWPPDNATCMISGLVQMSVSASVPTLVAIAVERFCRIVHPFREKL--TLKALVT 161  
 NL+ + F CK +G+SVS S +LVAIA+ER+ I P+ + + T A  
 Sbjct 115 NLWGTPIPGTTICKAVSYLNGVSVSSTLSLVAIALERYSAICRPLQARVQTRSHAARV 174  
 Query 162 IAVINWALLIMCPSAVTLTVTREHHFMVDARNRSYPLYSCHWAPKGMRRVYTTVLV 221  
 I W L+ L+M P V V + C WP +R+ + +L  
 Sbjct 175 IVATWLSGLLWPPVYTTVTPQVGRVLE-----QCVHRWPSARVRQGTWVSLLL 223  
 Query 222 SHITLAPLALIVVMYARIARL 243  
 Sbjct 224 LLLFFITPGVVMAYVGLISREL 245

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